

APPROVED	O.G. FIG.	
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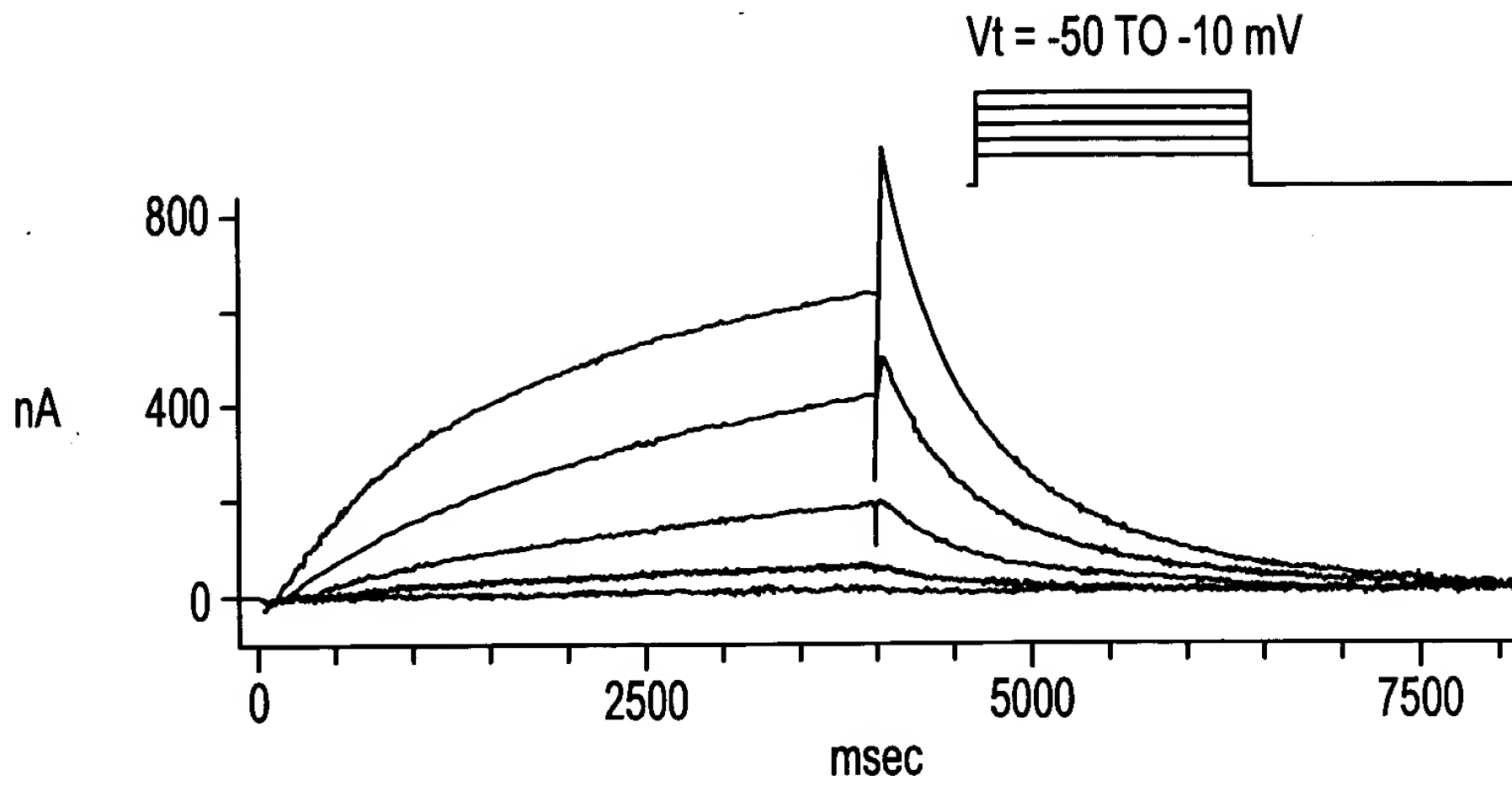


FIG. 1A

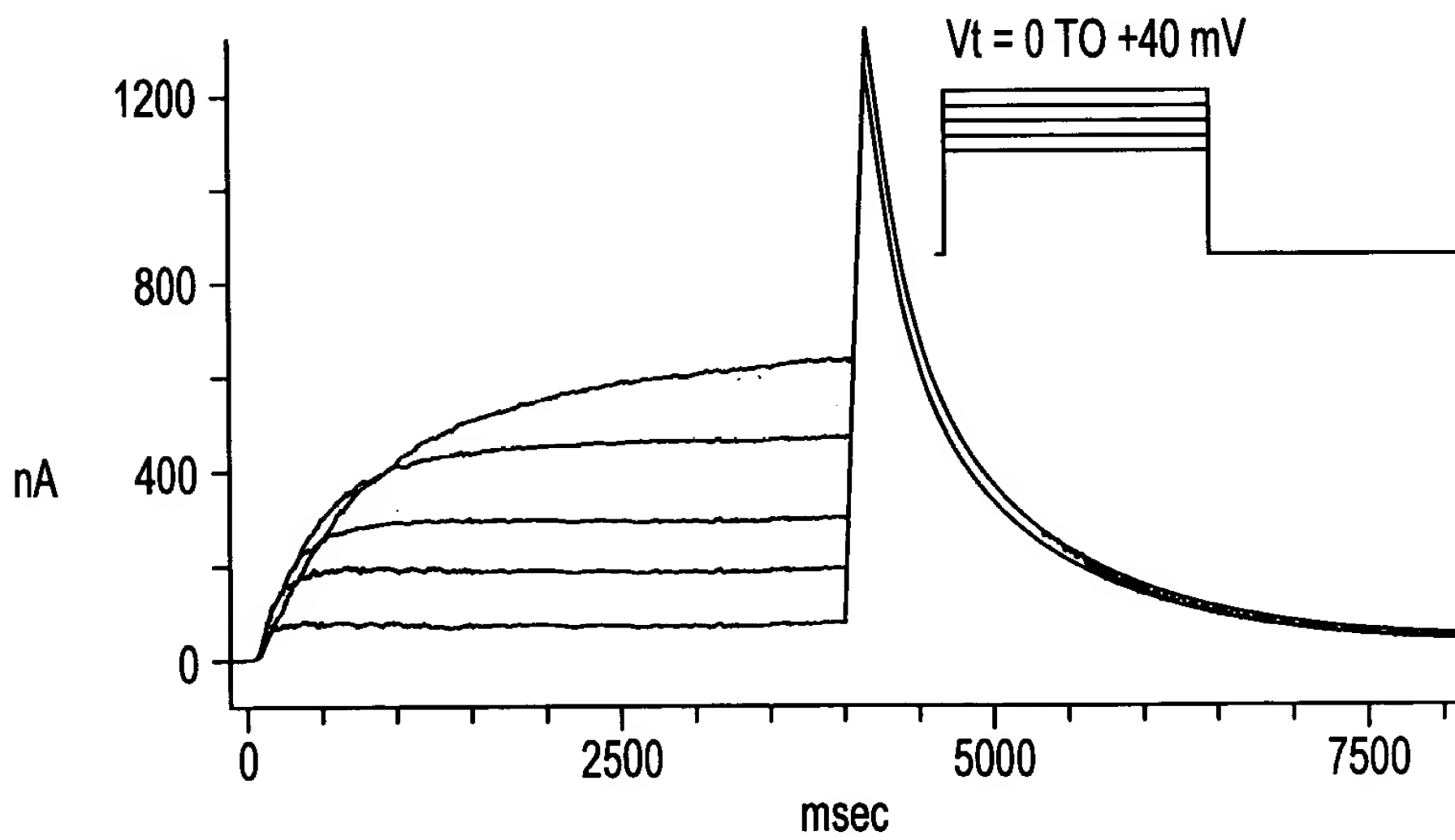


FIG. 1B

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004727-5665E260

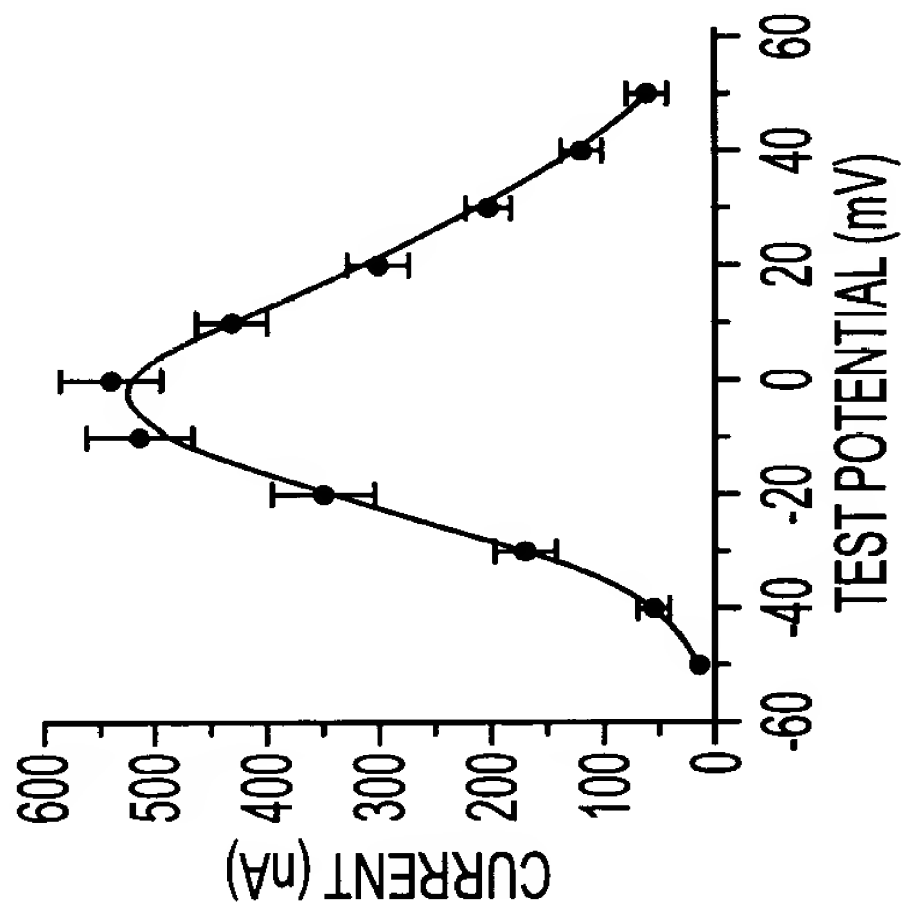


FIG. 1C

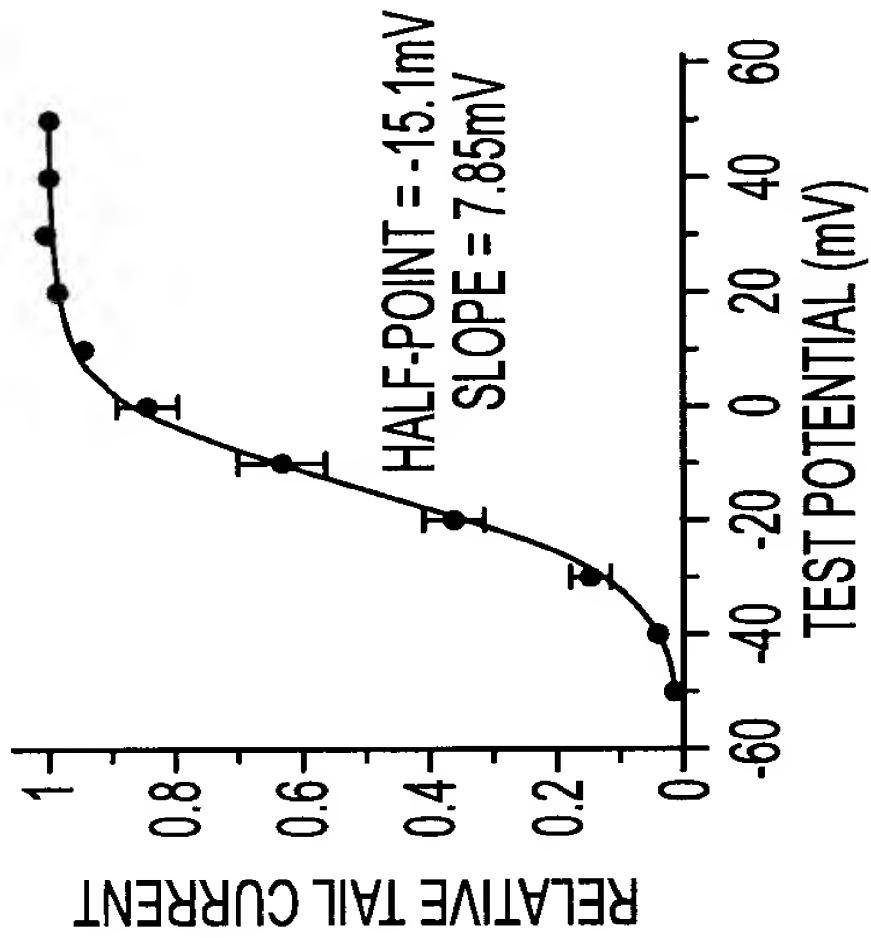


FIG. 1D

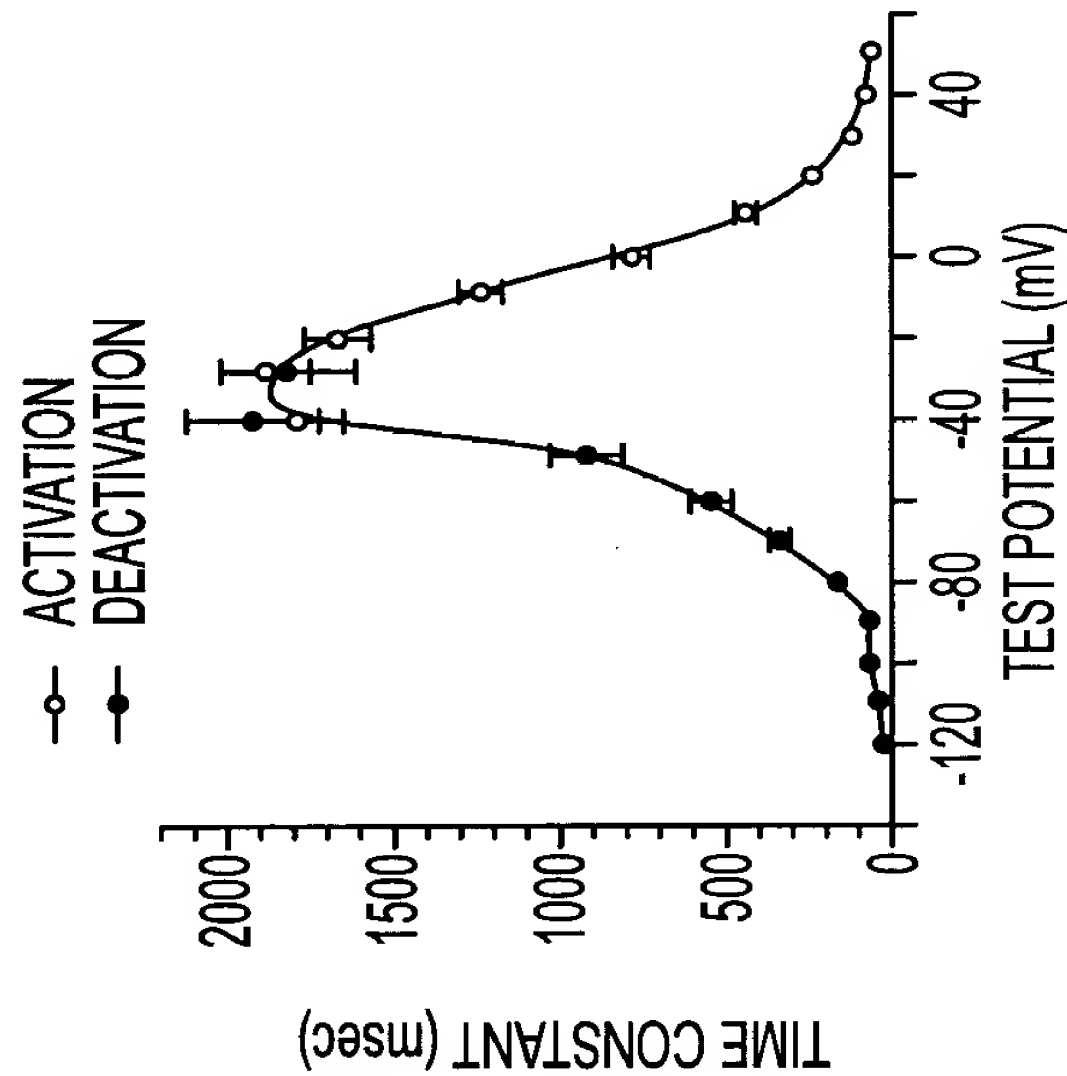


FIG. 2C

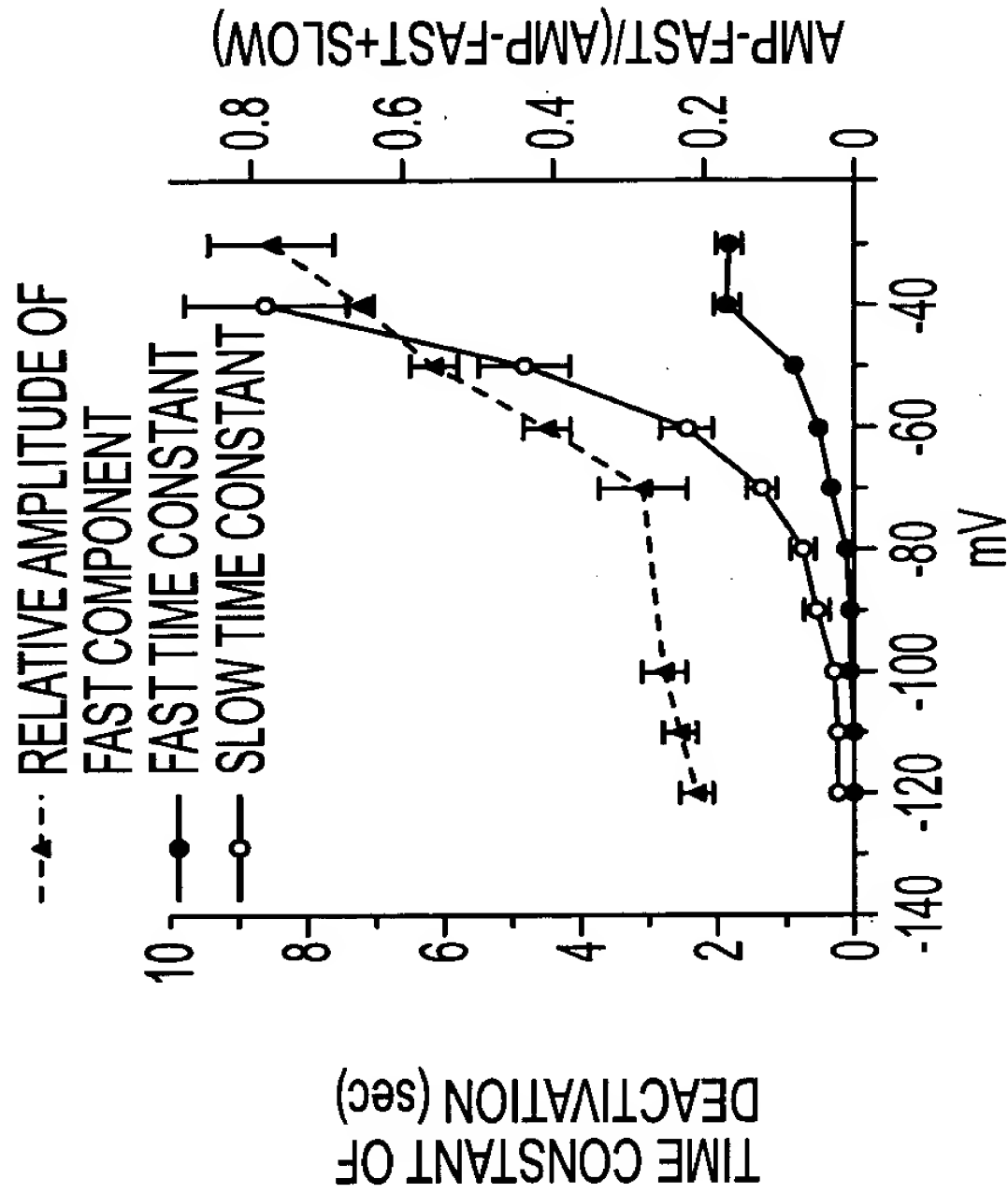


FIG. 2D

APPROVED	O.G. FIG.	
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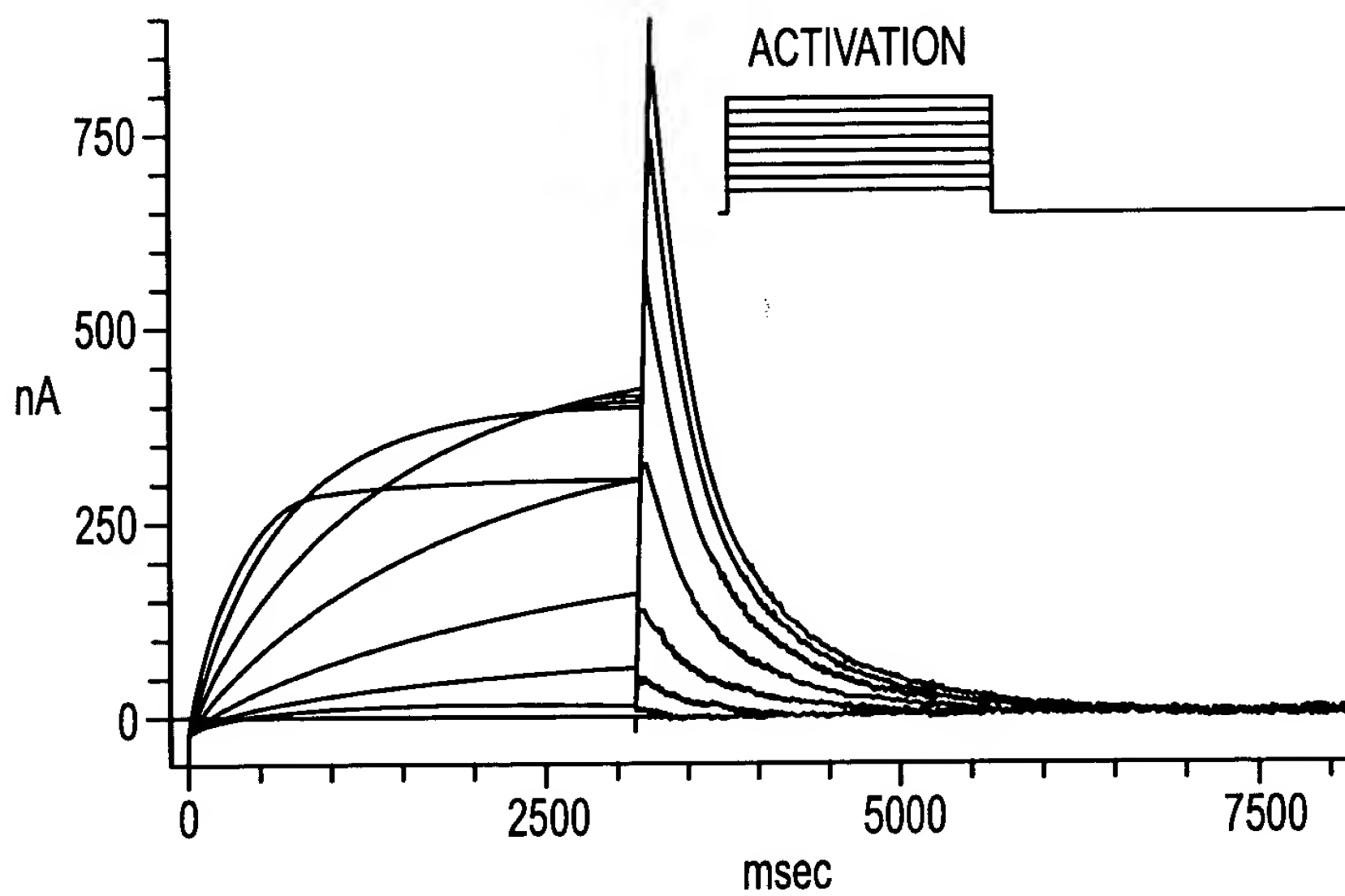


FIG. 2A

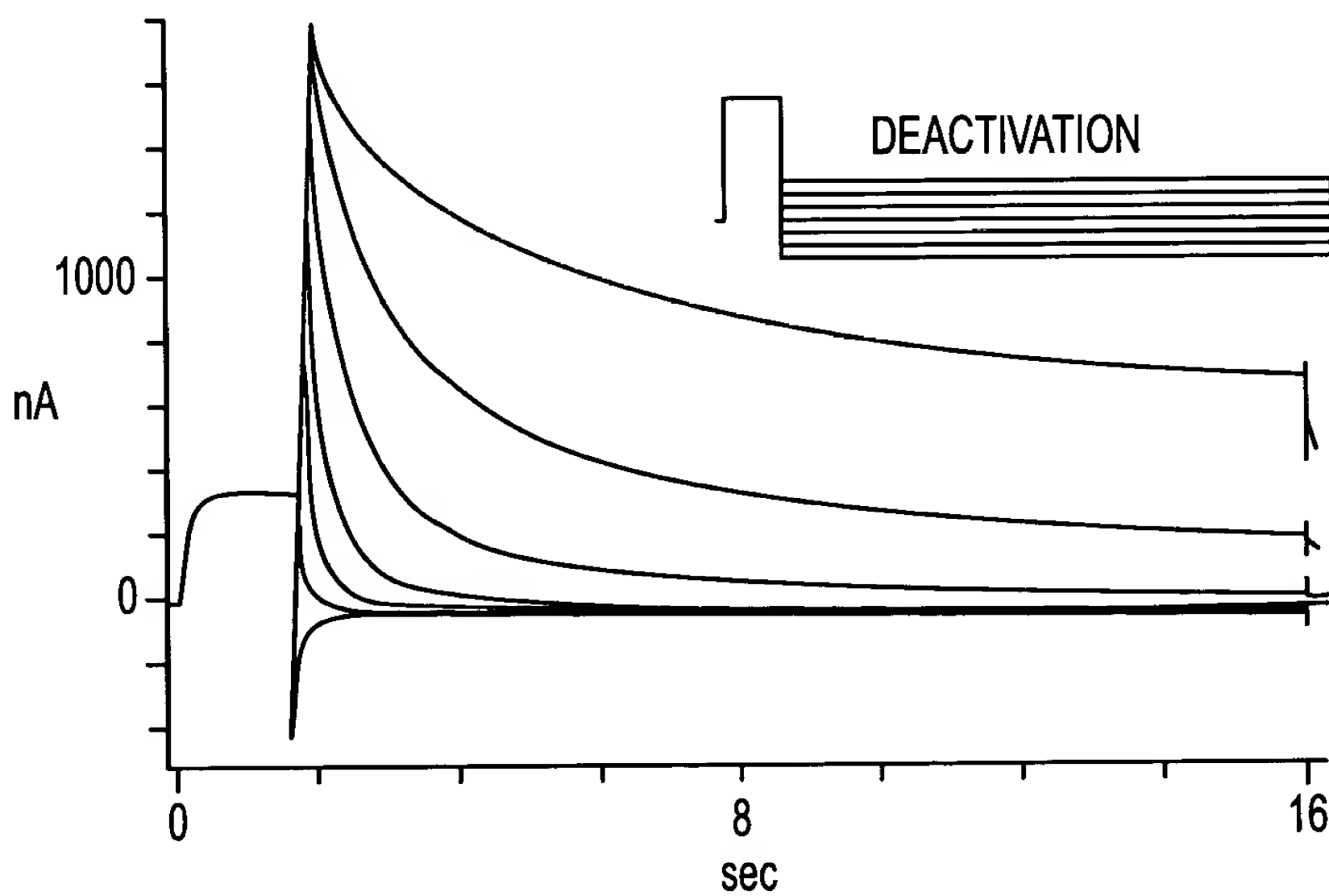


FIG. 2B

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APPROVED	O.G. FIG.	
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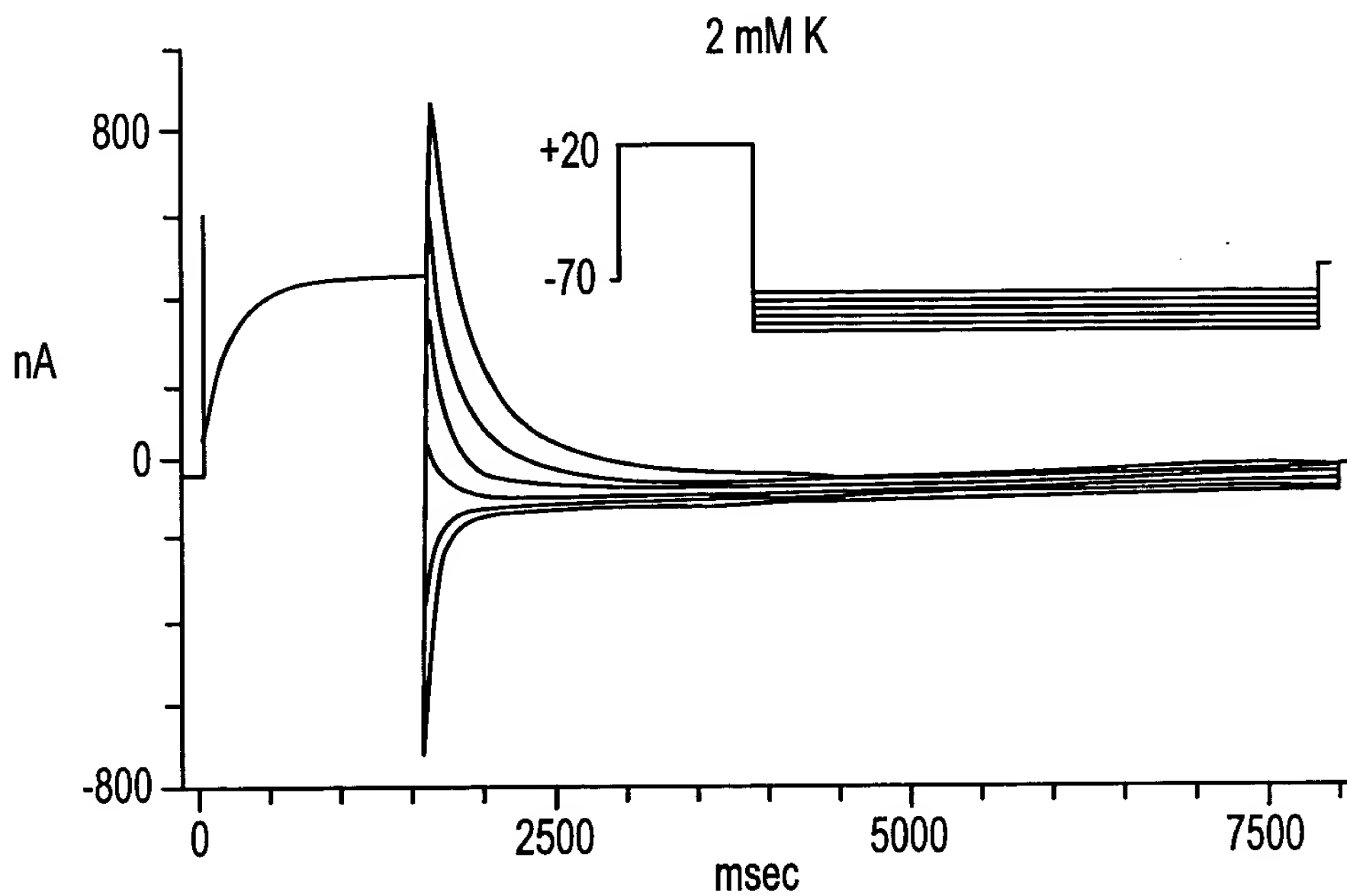


FIG. 3A

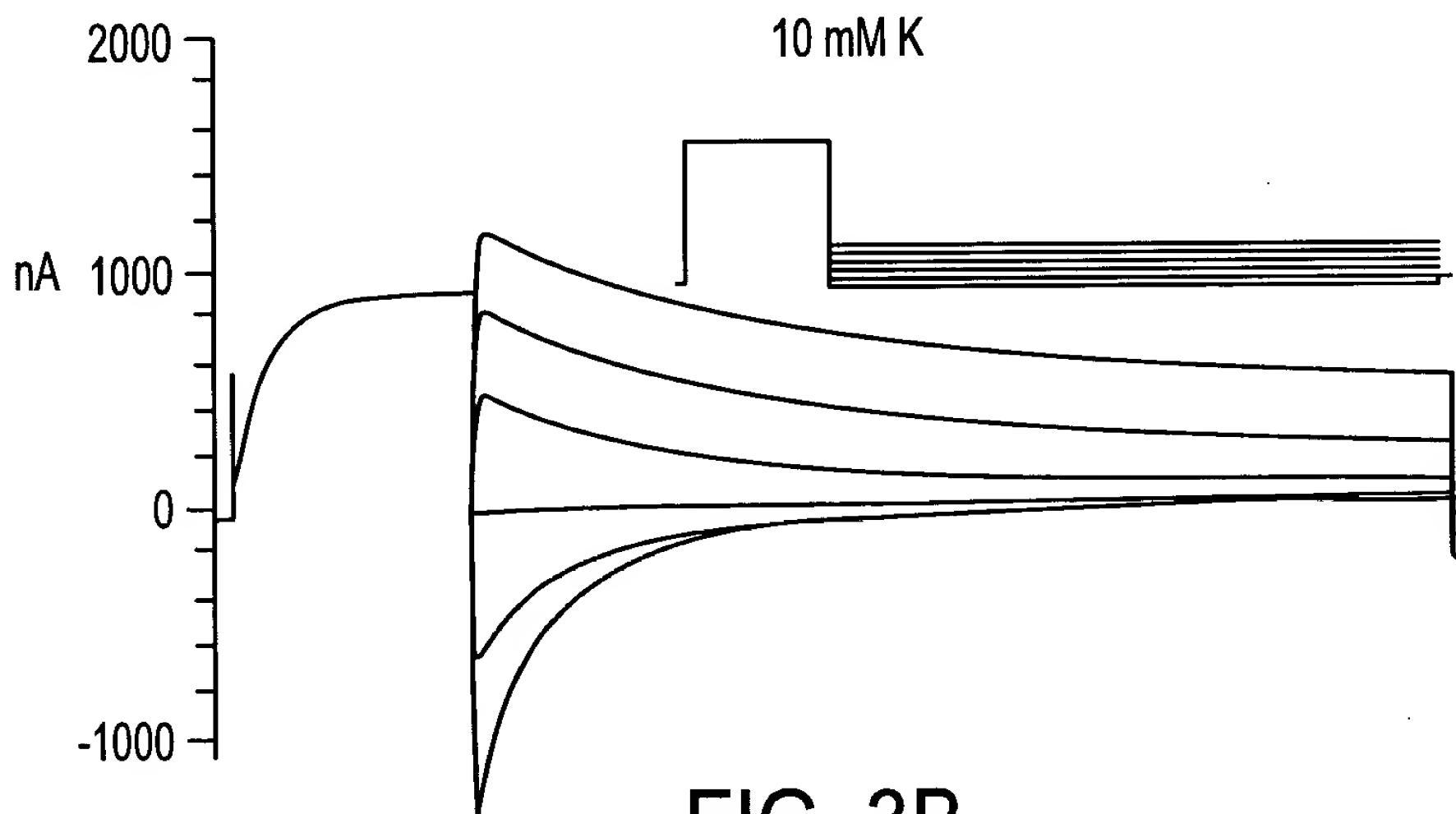


FIG. 3B

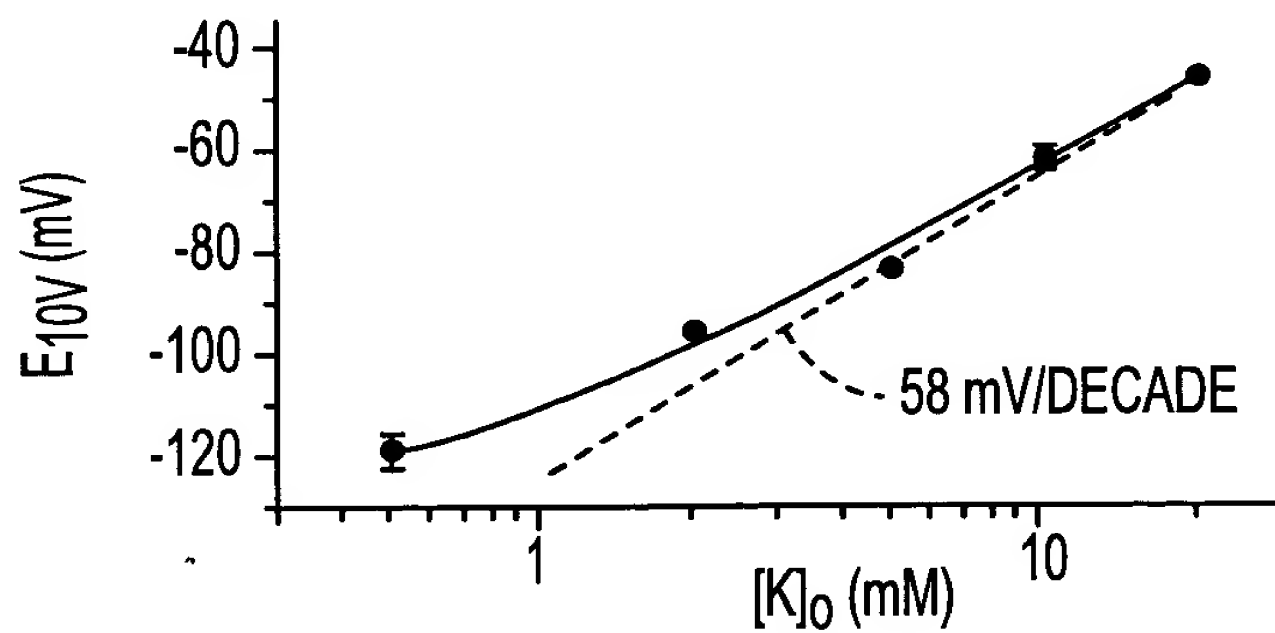


FIG. 3C

0075995-42400

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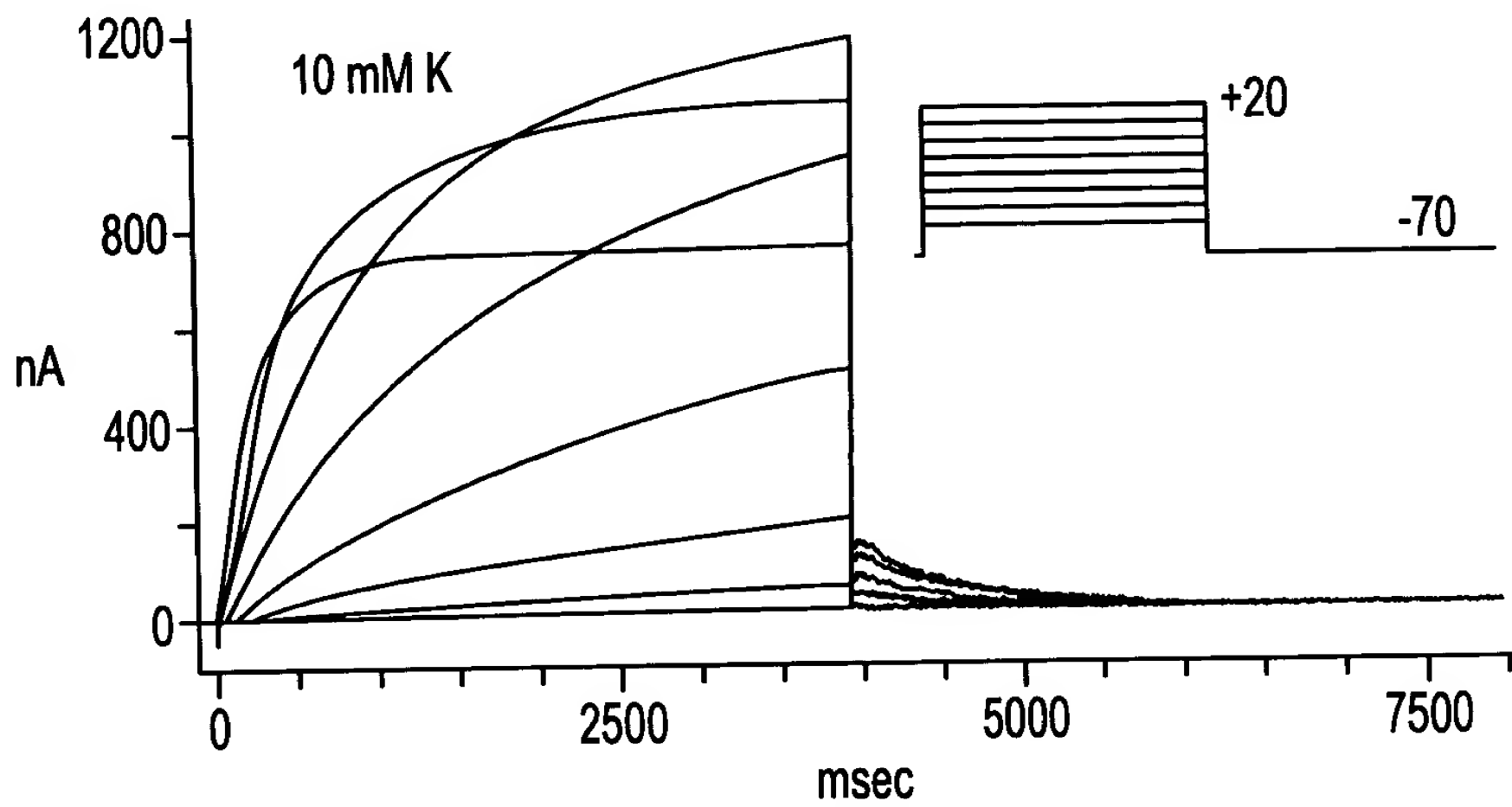


FIG. 4A

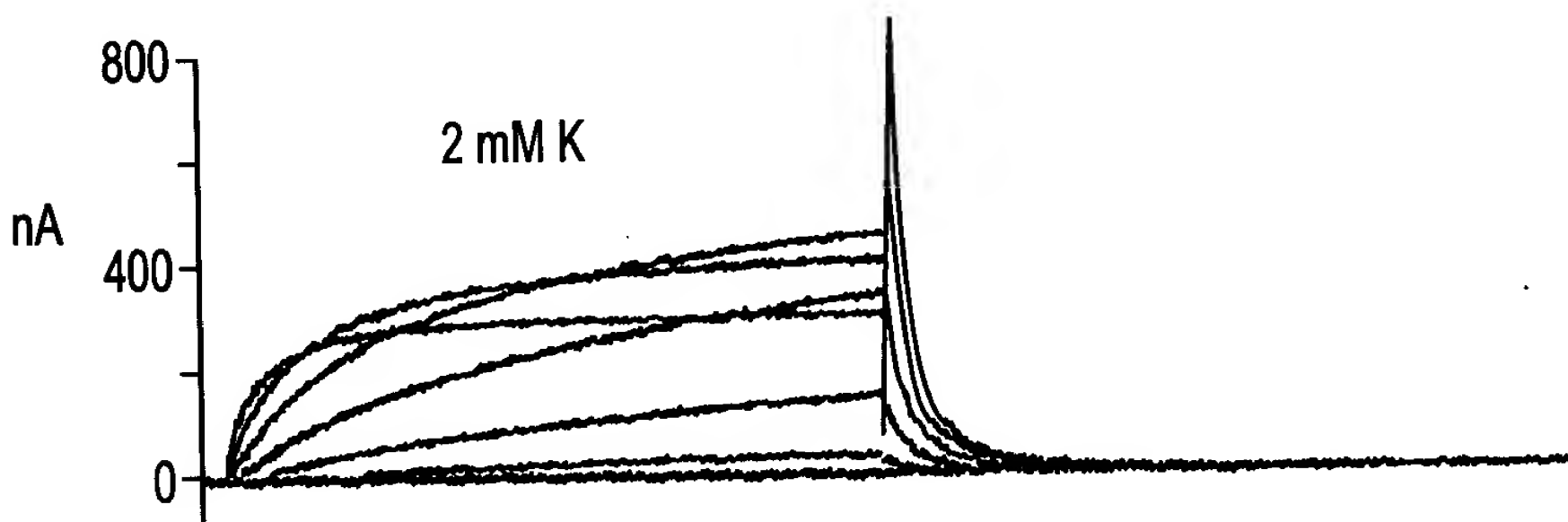


FIG. 4B

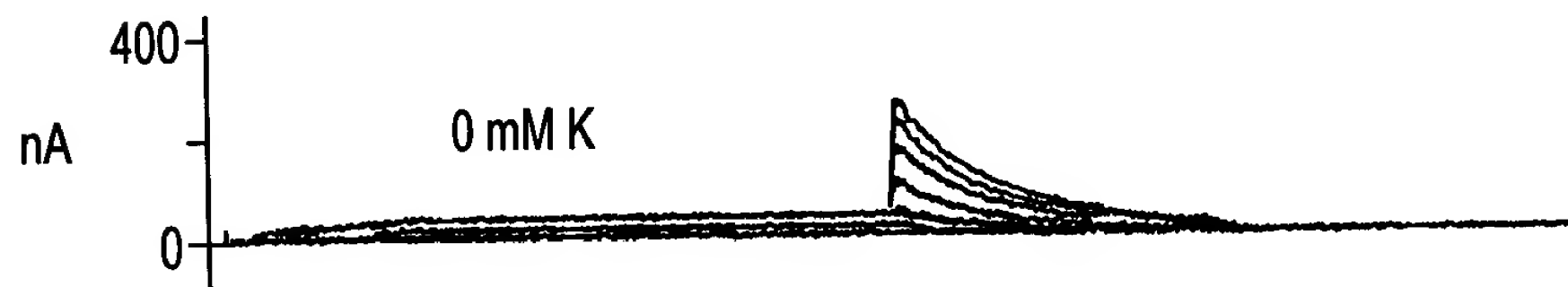


FIG. 4C

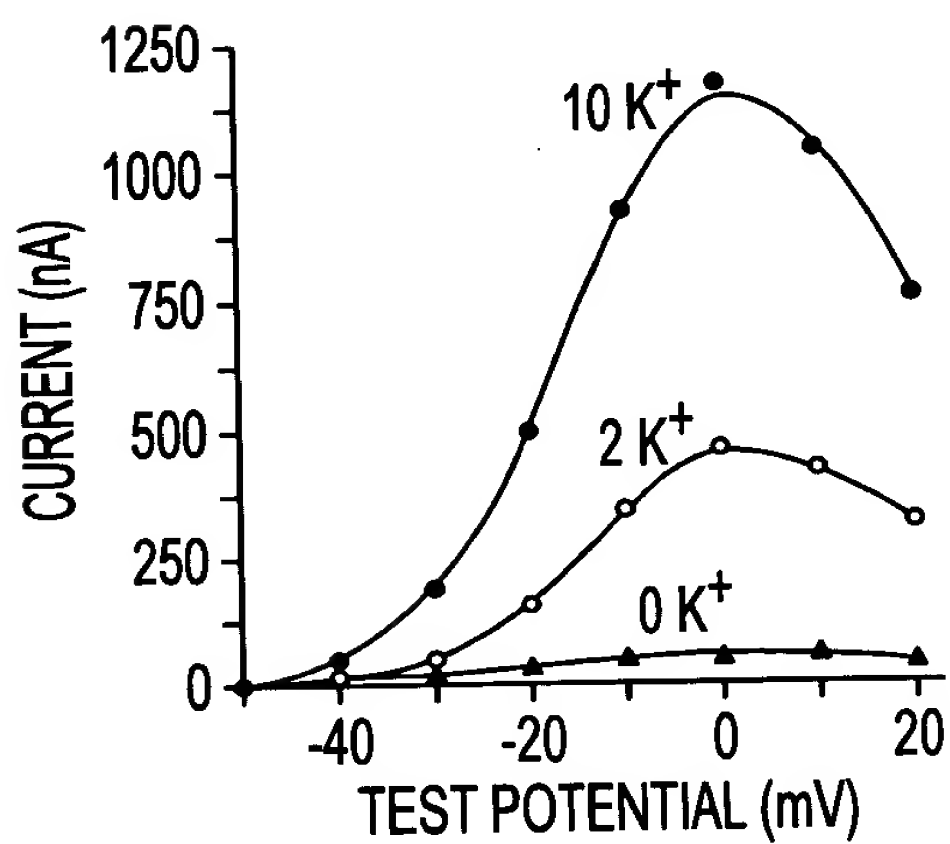


FIG. 4D

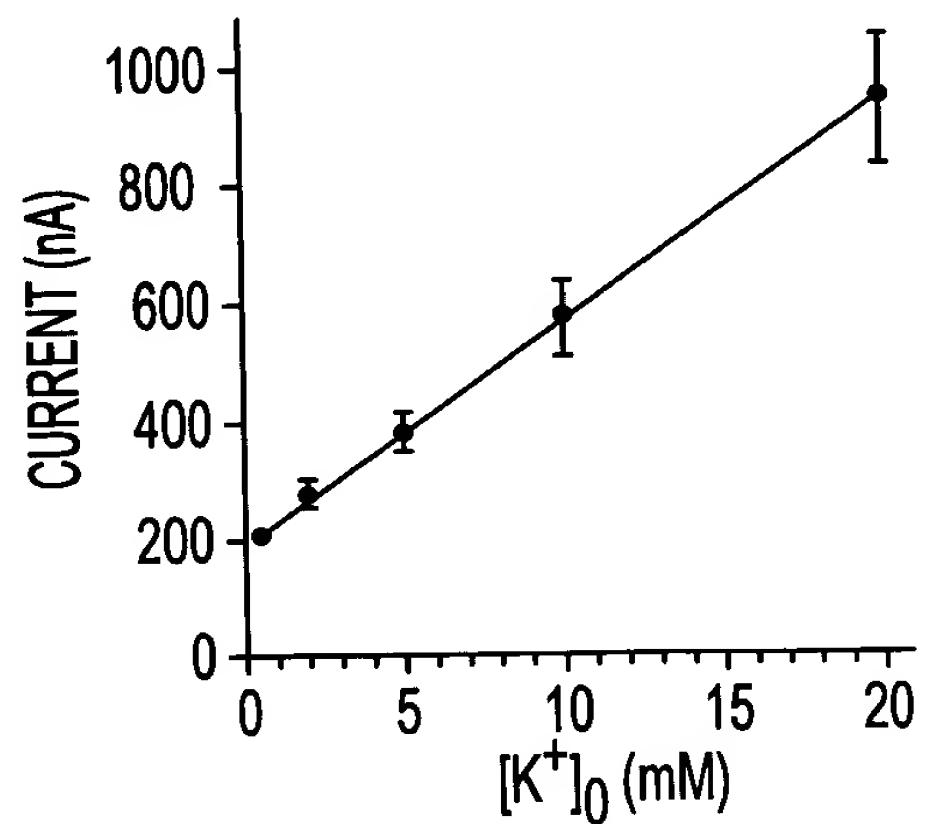


FIG. 4E

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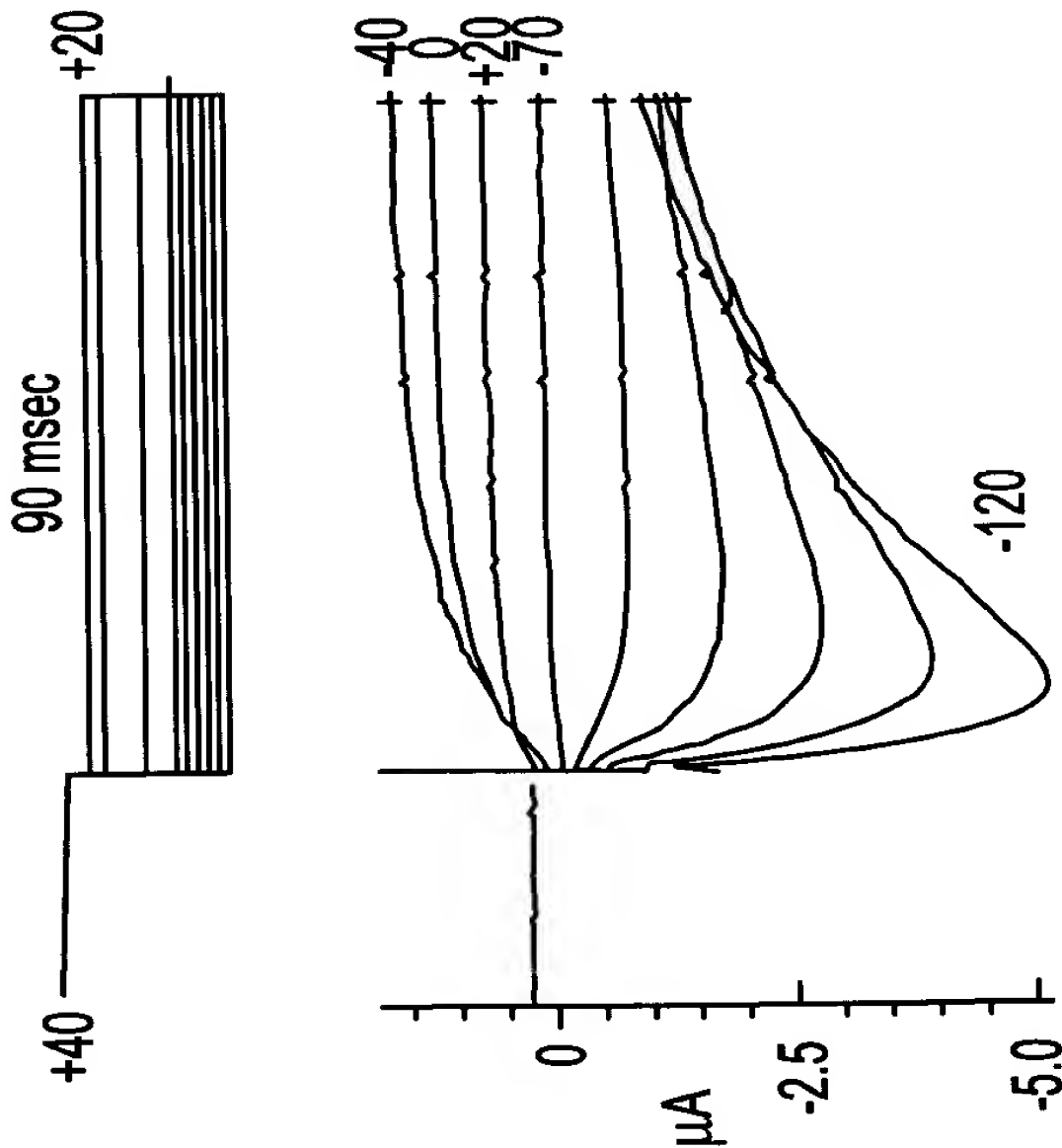


FIG. 5A

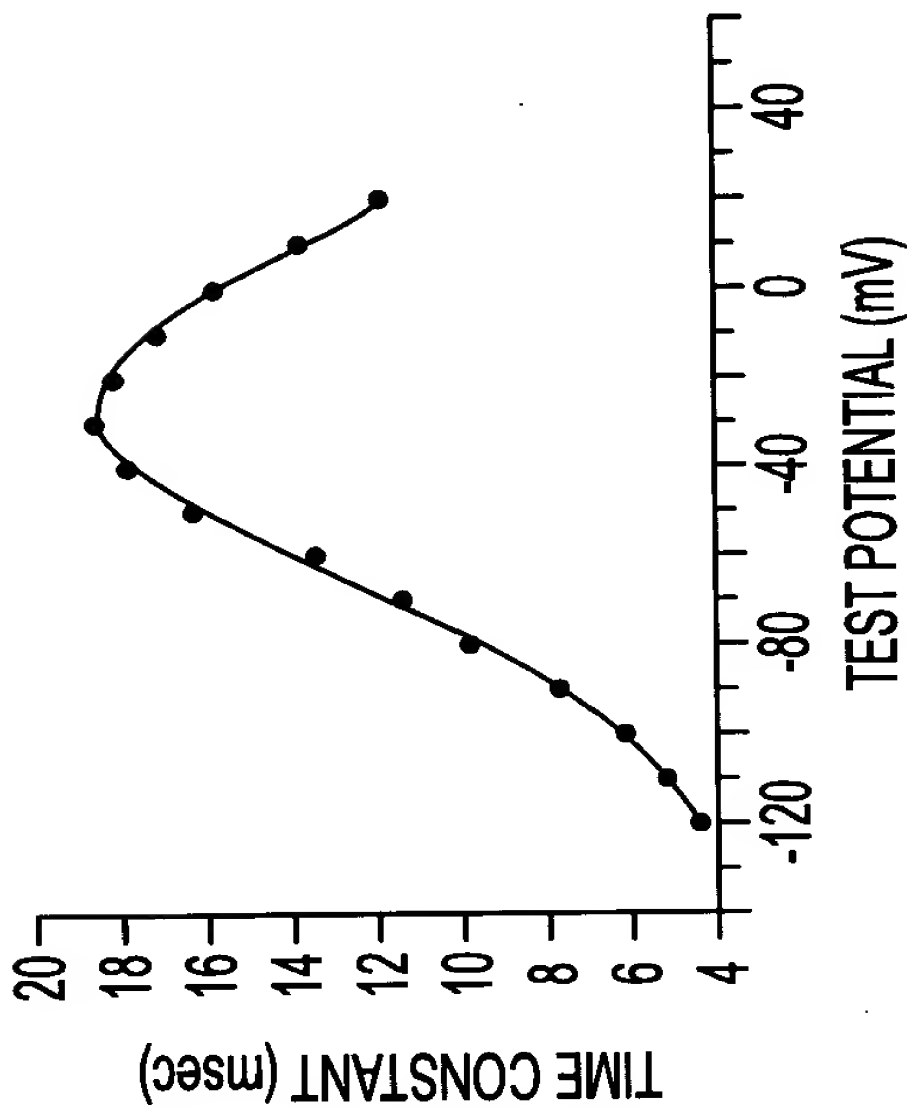


FIG. 5B



APPROVED	O.G. FIG.	
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Docket No.: 2323-156

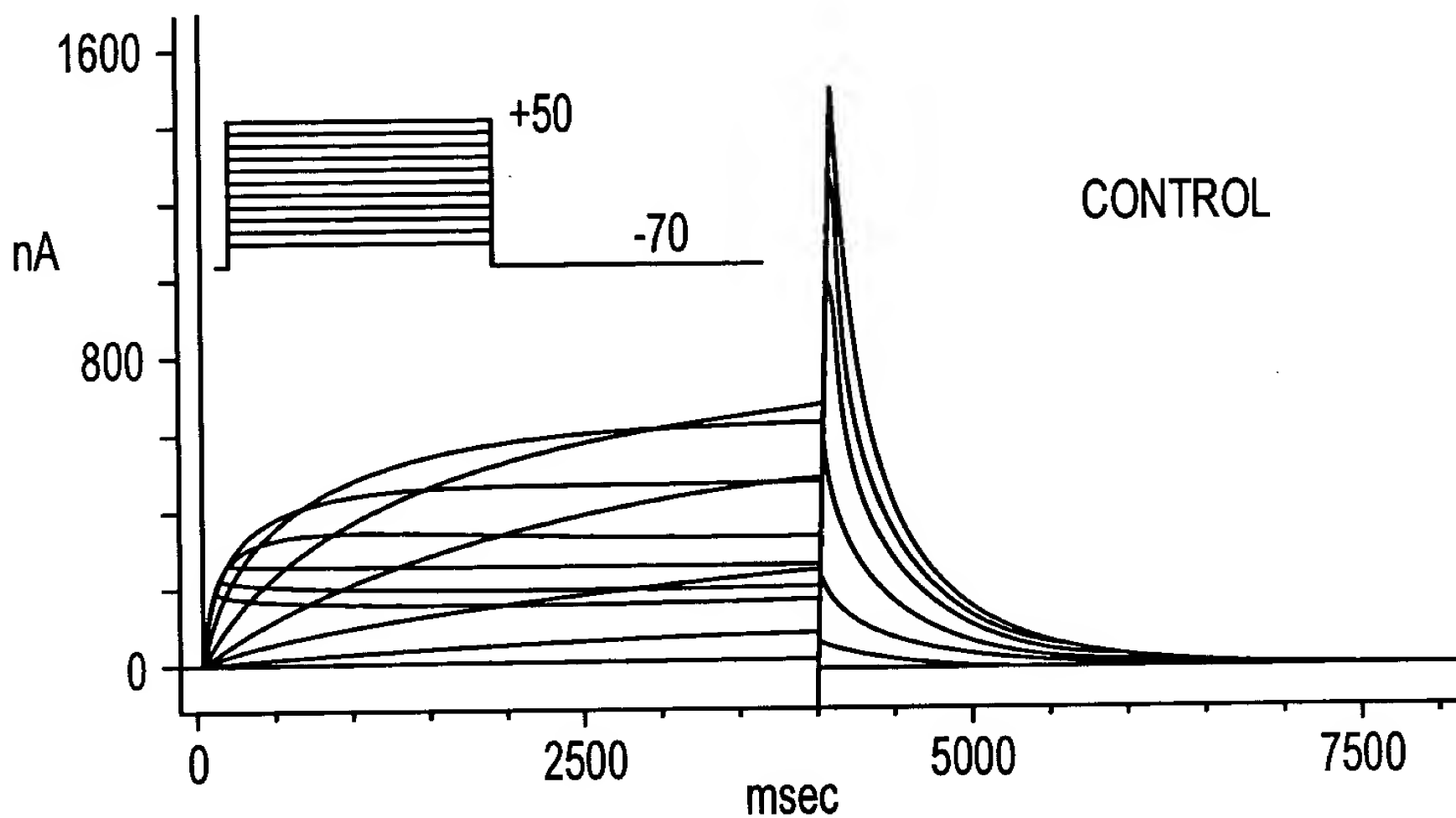


FIG. 6A

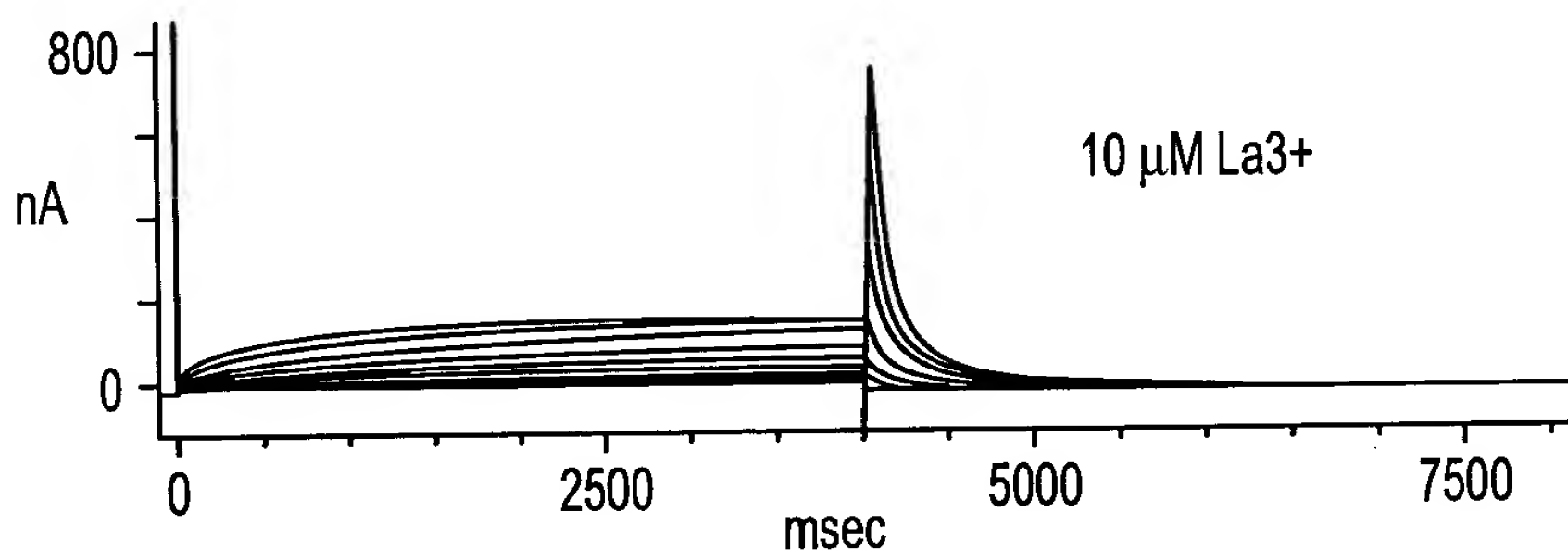


FIG. 6B

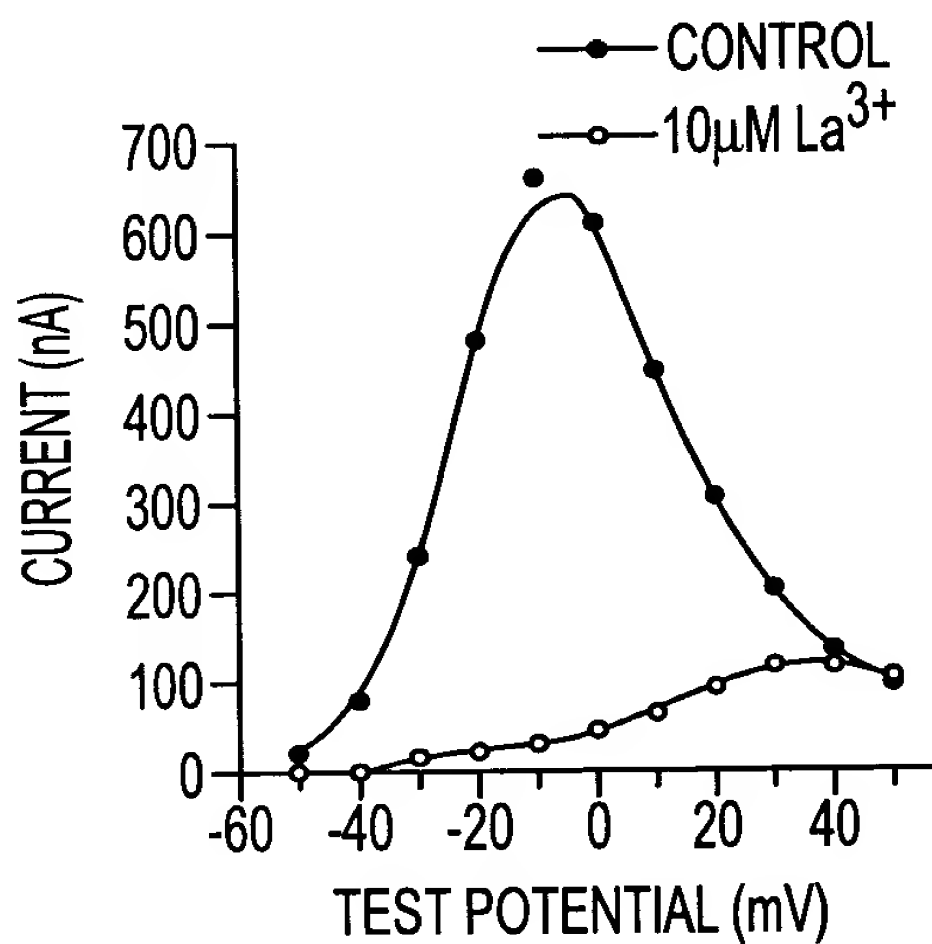


FIG. 6C

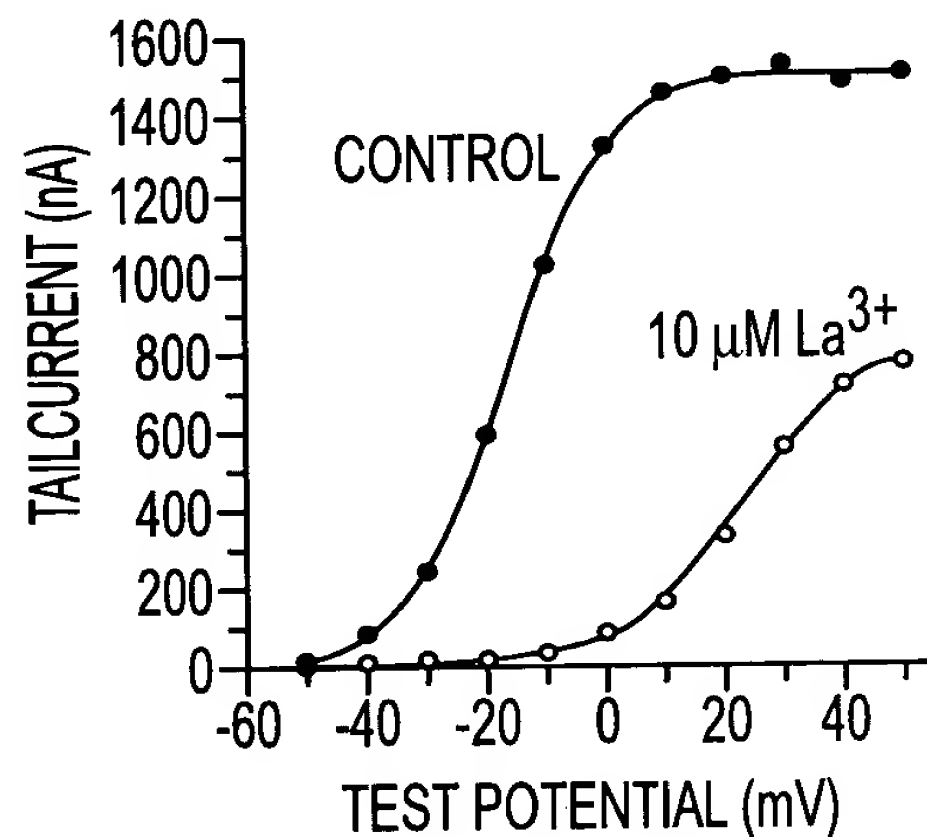


FIG. 6D



APPROVED	O.G. FIG.	
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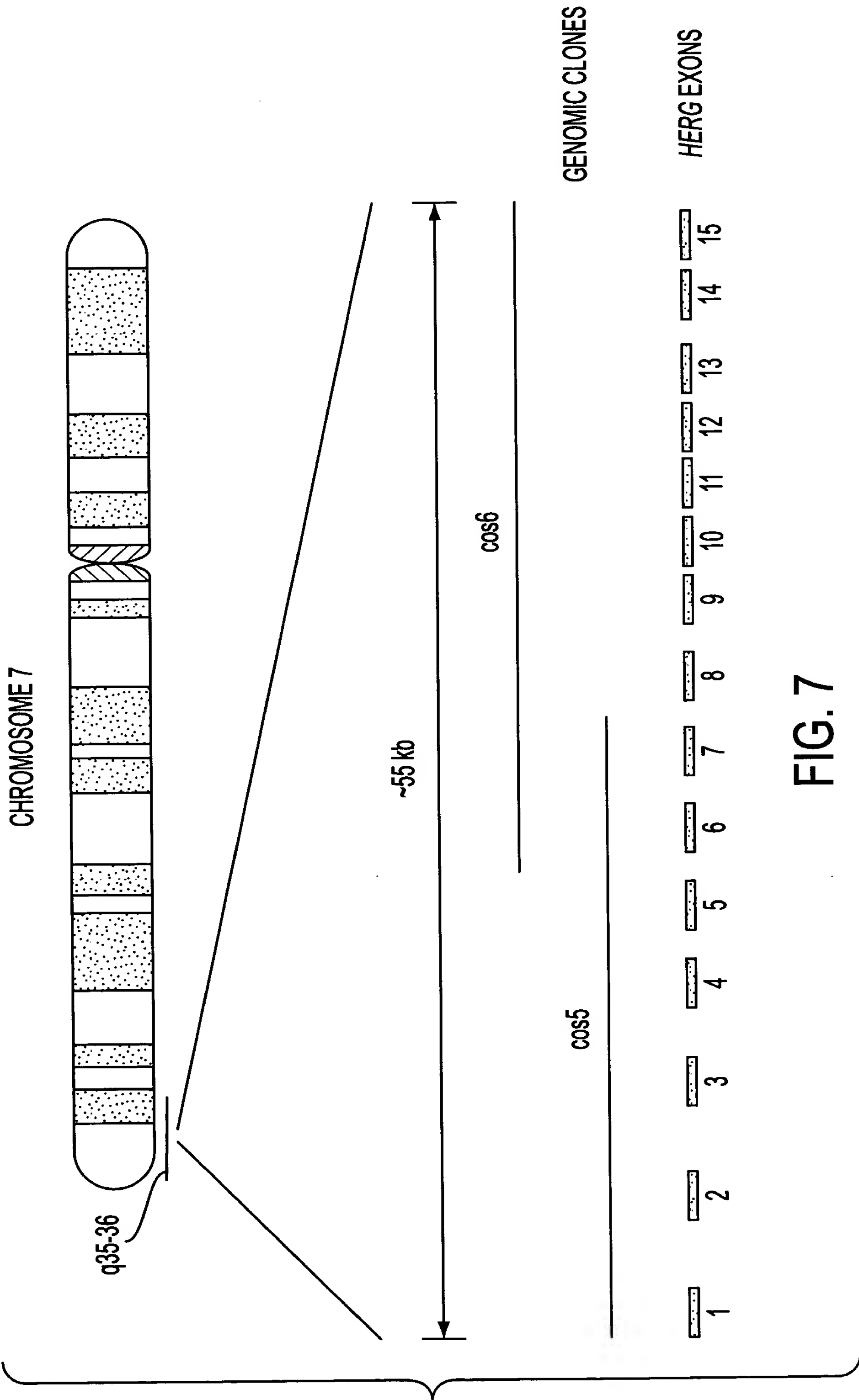


FIG. 8A

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APPROVED	O.G. FIG.	
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AGCATCTTCGGCAACGTGTCGGCCATCATCCAGCGGCTGTACTCGGGCACAGCCCGCTACCACACACAGATGCTGCGGGTG-2106  
S I F G N V S A I I O R L Y S G T A R Y H T Q M L R V -680

CGGGAGTTCATCCGCTTCCACCAGATCCCCAATCCCCTGCGCCAGCGCCTCGAGGAGTACTTCCAGCACGCCTGGTCCTAC-2187  
R E F I R F H Q I P N P L R Q R L E E Y F Q H A W S Y -707

▽

ACCAACGGCATCGACATGAACGCGGTGCTGAAGGGCTTCCCTGAGTGCCTGCAGGCTGACATCTGCCTGCACCTGAACCGC-2268  
T N G I D M N A V L K G F P E C L Q A D I C L H L N R -734  
TCACTGCTGCAGCACTGCAAACCTTCCGAGGGGCCACCAAGGGCTGCCTTCGGGCCCTGGCCATGAAGTTCAAGACCACA-2349  
S L L Q H C K P F R G A T K G C L R A L A M K F K T T -761  
CATGCACCGCCAGGGGACACACTGGTGCATGCTGGGGACCTGCTCACCGCCCTGTACTTCATCTCCCGGGGCTCCATCGAG-2430  
H A P P G D T L V H A G D L L T A L Y F I S R G S I E -788

▽

ATCCTGCGGGGCGACGTCGTCGTGGCCATCCTGGGGAAGAATGACATCTTTGGGGAGCCTCTGAACCTGTATGCAAGGCCT-2511  
I L R G D V V V A I L G K N D I F G E P L N L Y A R P -815

cNBD

GGCAAGTCGAACGGGGATGTGCGGGCCCTCACCTACTGTGACCTACACAAGATCCATCGGGACGACCTGCTGGAGGTGCTG-2592  
G K S N G D V R A L T Y C D L H K I H R D D L L E V L -842

▽

GACATGTACCCTGAGTTCTCCGACCACTTCTGGTCCAGCCTGGAGATCACCTTCAACCTGCGAGATACCAACATGATCCCG-2673  
D M Y P E F S D H F W S S L E I T F N L R D T N M I P -869  
GGCTCCCCCGGCAGTACGGAGTTAGAGGGTGGCTTCAGTCGGCAACGCAAGCGCAAGTTGTCCTTCCGCAGGCGCACGGAC-2754  
G S P G S T E L E G G F S R Q R K R K L S F R R R T D -896

▽

AAGGACACGGAGCAGCCAGGGGAGGTGTGCGCCTTGGGGCCGGGCGGGGCGGGGCGAGTAGCCGGGGCCGGCCG-2835  
K D T E Q P G E V S A L G P G R A G A G P S S R G R P -923  
GGGGGGCCGTGGGGGAGAGCCCGTCCAGTGGCCCTCCAGCCCTGAGAGCAGTGAAGGATGAGGGCCAGGCCGACGCTCC-2916  
G G P W G E S P S S G P S S P E S S E D E G P G R S S -950  
AGCCCCCTCCGCTGGTGCCCTTCTCCAGCCCCAGGCCCCCGGAGAGCCGCGGGTGGGGAGCCCTGATGGAGGACTGC-2997  
S P L R L V P F S S P R P P G E P P G G E P L M E D C -977

▽

GAGAAGAGCAGCGACACTTGCAACCCCCTGTGAGGCGCCTTCTCAGGAGTGTCCAACATTTTCAGCTTCTGGGGGGACAGT-3078  
E K S S D T C N P L S G A F S G V S N I F S F W G D S -1004  
CGGGGCCCGCAGTACCAGGAGCTCCCTCGATGCCCCGCCCCACCCCCAGCCTCCTCAACATCCCCCTCTCCAGCCCGGGT-3159  
R G R Q Y Q E L P R C P A P T P S L L N I P L S S P G -1031

▽

CGGCGGCCCCGGGGCGACGTGGAGAGCAGGCTGGATGCCCTCCAGCGCCAGCTCAACAGGCTGGAGACCCGGCTGAGTGCA-3240  
R R P R G D V E S R L D A L Q R Q L N R L E T R L S A -1058  
GACATGGCCACTGTCCTGCAGCTGCTACAGAGGAGATGACGCTGGTCCCGCCCGCCTACAGTGTGTGACCACCCCGGGG-3321  
D M A T V L Q L L Q R Q M T L V P P A Y S A V T T P G -1085

▽

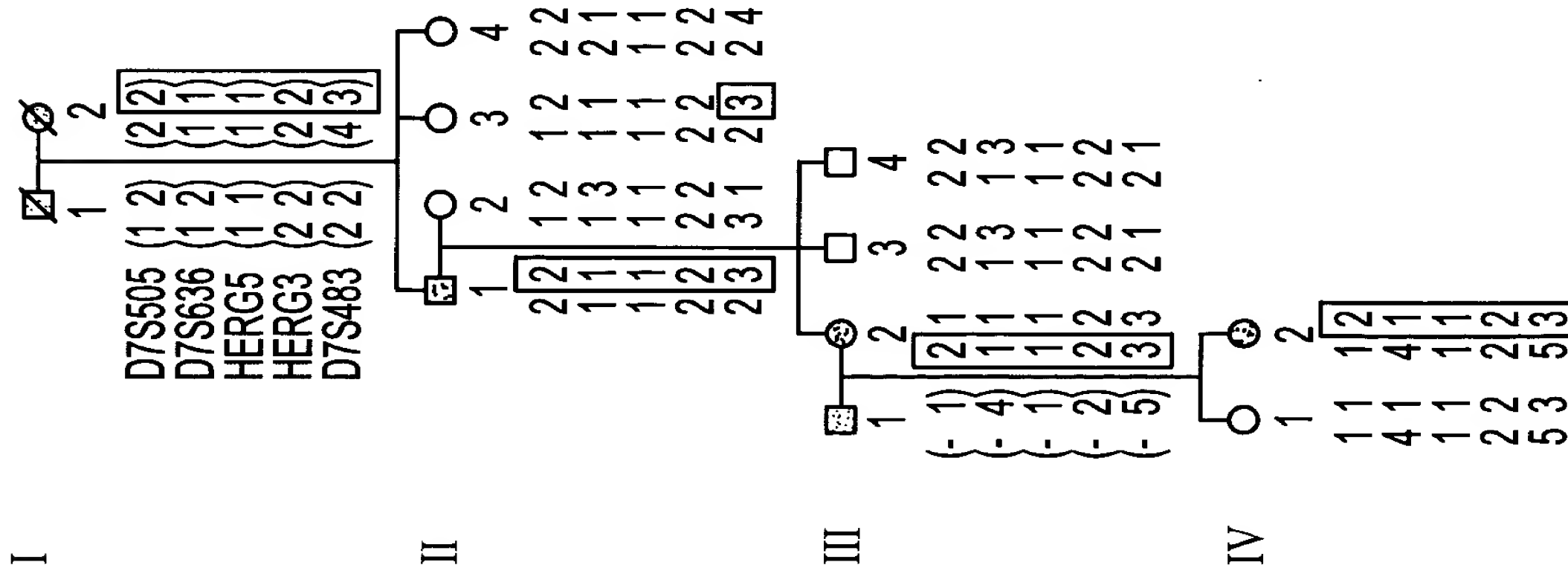
CCTGGCCCCACTTCCACATCCCCGCTGTTGCCCGTCAGCCCCCTCCCCACCTCACCTTGGACTCGCTTTCTCAGGTTTCC-3402  
P G P T S T S P L L P V S P L P T L T L D S L S Q V S -1112  
CAGTTCATGGCGTGTGAGGAGCTGCCCCCGGGGGCCCCAGAGCTTCCCCAAGAAGGCCCCACACGACGCTCTCCCTACCG-3483  
Q F M A C E E L P P G A P E L P Q E G P T R R L S L P -1139  
GGCCAGCTGGGGGCCCTCACCTCCAGCCCCCTGCACAGACACGGCTCGGACCCGGGCAGTTAGTGGGGCTGCCAGTGTGG-3564  
G Q L G A L T S Q P L H R H G S D P G S \* -1159  
ACACGTGGCTCACCCAGGGATCAAGGCGCTGCTGGGGCCGCTCCCCTTGGAGGCCCTGCTCAGGAGGCCCTGACCGTGGAAG-3645  
GGGAGAGGAACTCGAAAGCACAGCTCCTCCCCAGCCCTTGGGACCATCTTCTCCTGCAGTCCCCTGGGCCCCAGTGAGAG-3726  
GGGCAGGGGCGAGGCGGCGAGTGGTGGGGCCTGTGGTCCCCCACTGCCCTGAGGGCATTAGCTGGTCTAACTGCCCGGA-3807  
GGCACCCGGCCCTGGGCCCTTAGGCACCTCAAGGACTTTTCTGCTATTTACTGCTCTTATTGTAAAGGATAATAATTAAGGA-3888  
TCATATGAATAATTAATGAAGATGCTGATGACTATGAATAATAATAATTATCCTGAGGAG (A)n -3949

FIG. 8B

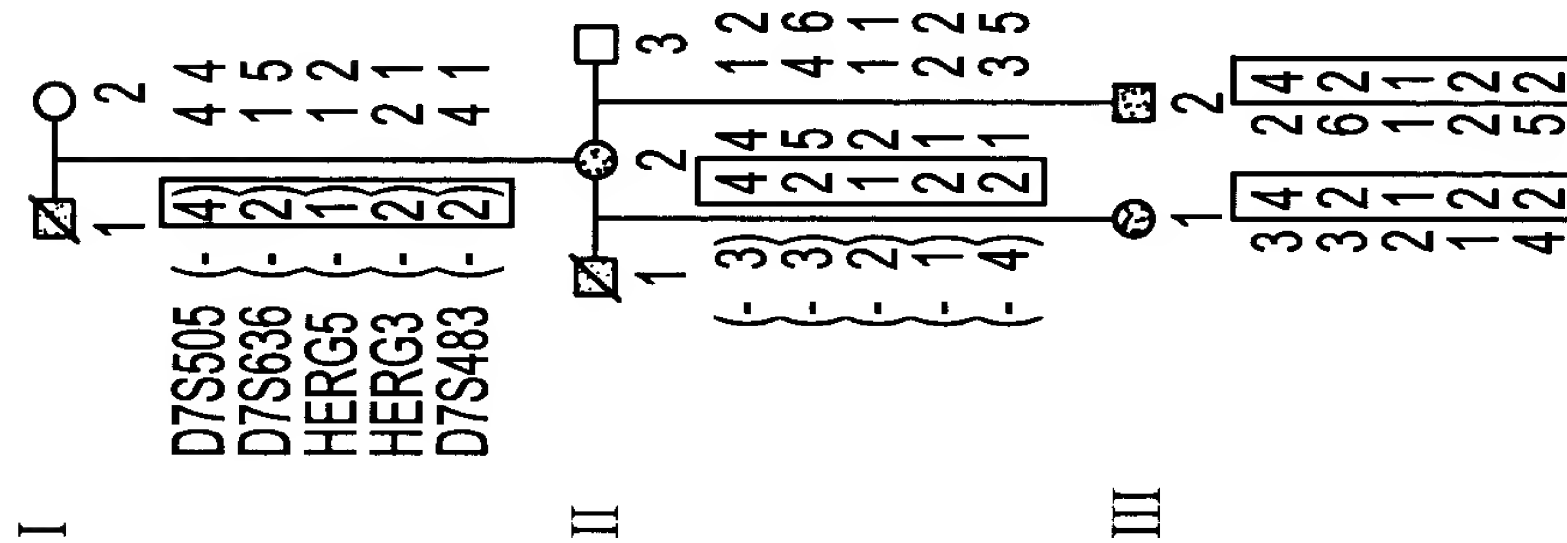


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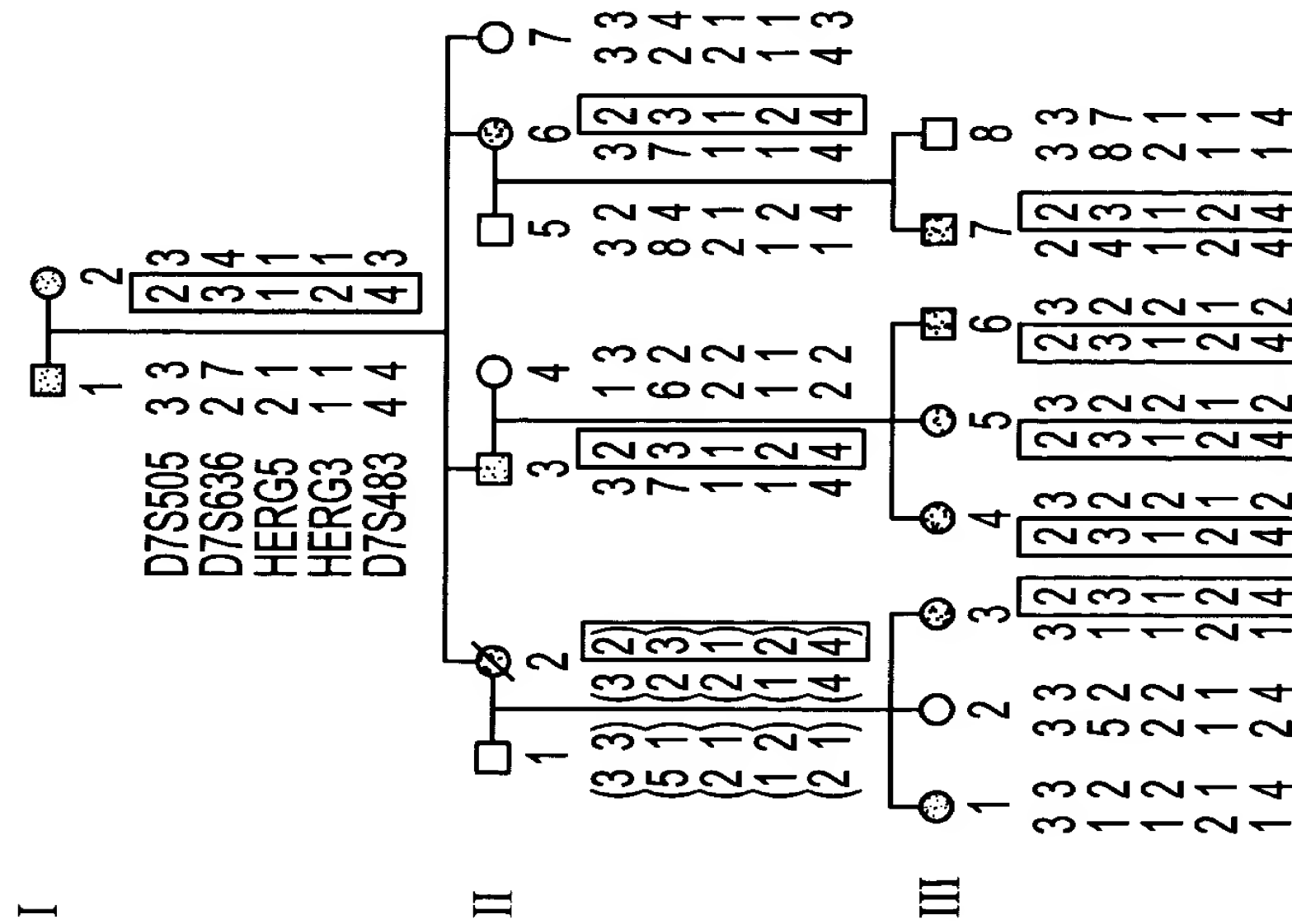
K2595



K2596



K2600



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TGG TTC CTC ATC GAC ATG GTG GCC GCC ATC CCC TTC GAC CTG CTC SEQ ID NO:96  
W F L I D M V A A I P F D L L SEQ ID NO:97  
S3

FIG. 10C

NORMAL      GTC ATC TAC ACG GCT GTC TTC ACA CCC TAC TCG GCT GCC TTC CTG CTG AAG GAG SEQ ID NO:98  
              V I Y T A V F T P Y S A A F L L K E SEQ ID NO:99

DELETION    GTC ATC TAC CGG CTG TCT TCA CAC CCT ACT CGG CTG CCT TCC TGC TGA SEQ ID NO:100  
              V I Y R L S S S H P T R L P S C SEQ ID NO:101

FIG. 11C

APPROVED	O.G. FIG.	
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	GTG→V	SEQ ID
	GCG	NO:
	\\	
	L I A H W L	102
	↔S5↔	
K1956	L I V H W L	103
H-Erg	L I A H W L	102
M-Eag	L A A H W K	104
R-Eag	L A A H W M	105
Eag	L V A H W L	106
Elk	L A A H W L	107

FIG. 12G

	GAC→D	SEQ ID
	AAC	NO:
	\\	
	D I L I N F R	108
	↔S2↔	
K2596	D I L I D F R	109
H-Erg	D I L I N F R	108
M-Eag	D I V L N F H	110
R-Eag	D I V L N F H	110
Eag	D I V L N F H	110
Elk	D I L L N F R	111

FIG. 12H

5'-CAT CCT GG // gtagggg-3'  
C ↓

FIG. 12I



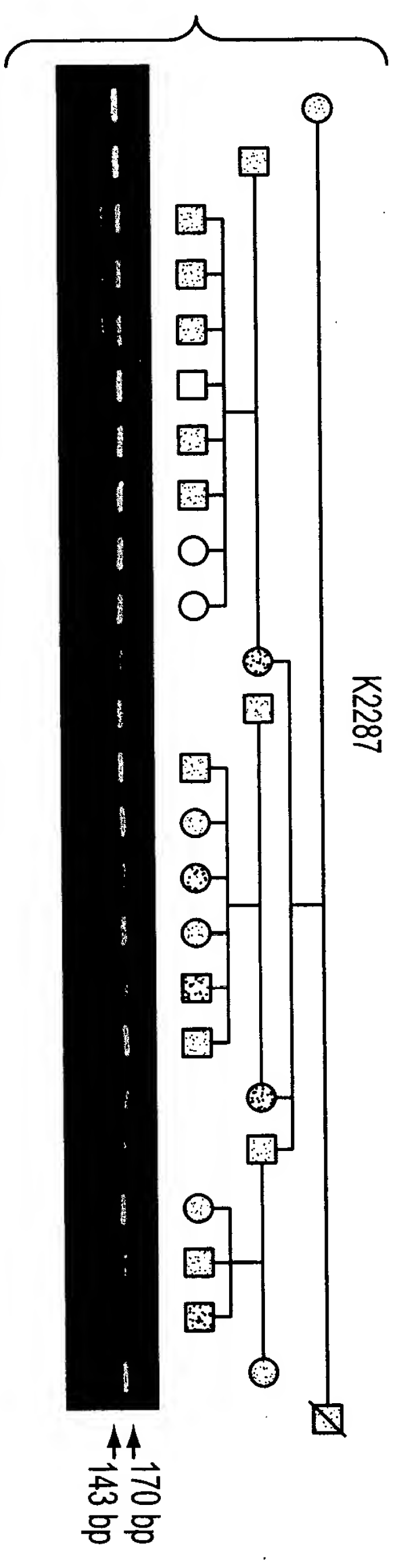


FIG. 10A

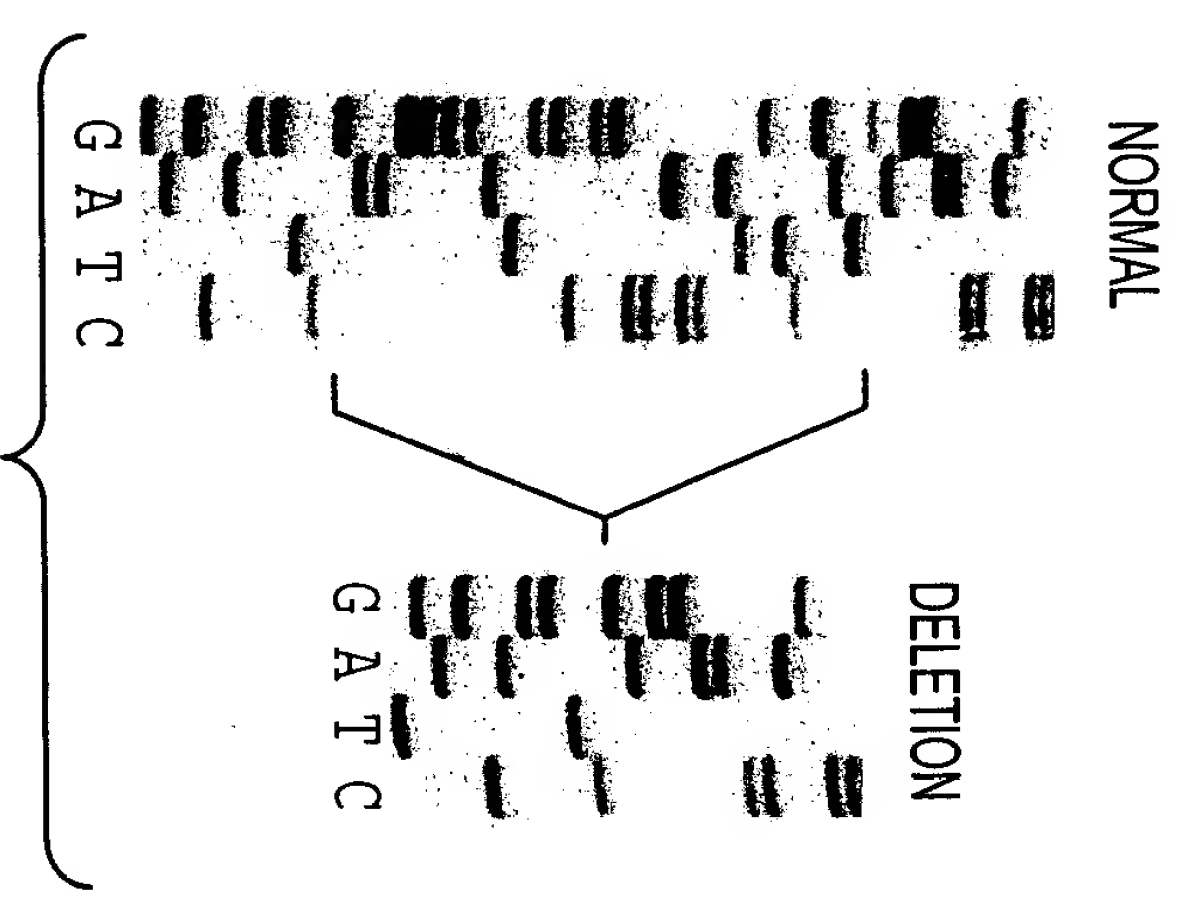


FIG. 10B



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APPROVED	T.G. FIG.	
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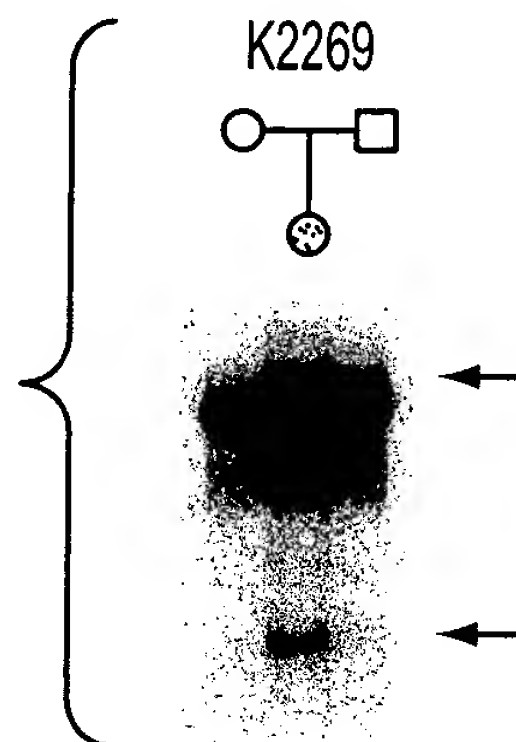


FIG. 14A

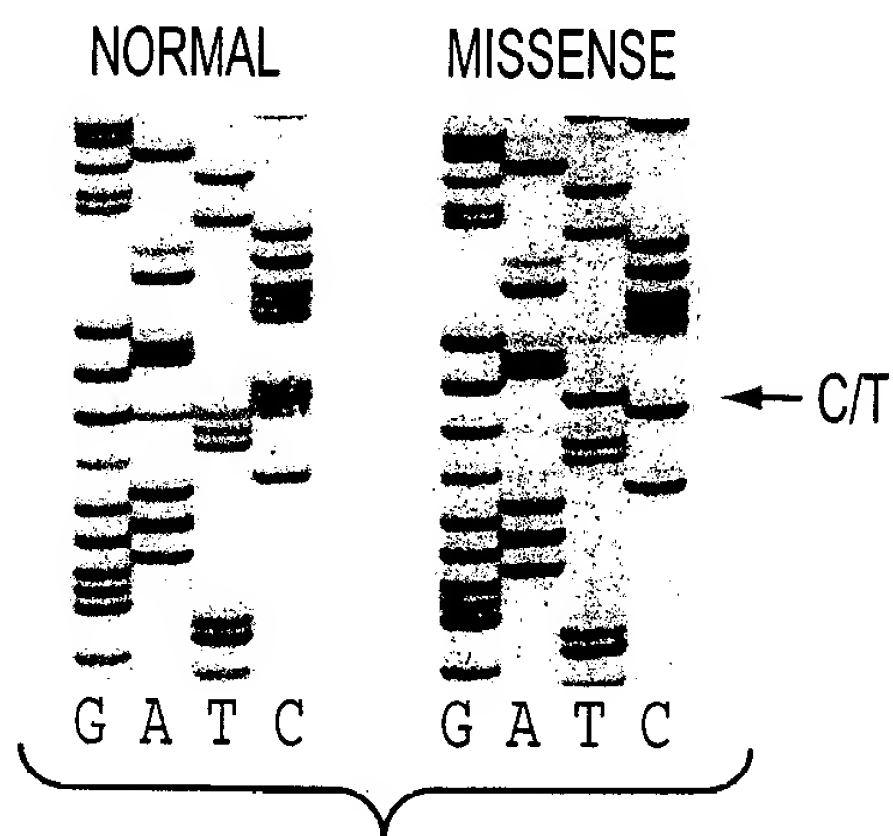


FIG. 14B

	AGC → S	SEQ ID
	GGC	NO:
	SVGFGNVS	112
	← PORE →	
K2269	SVGFSNVS	113
H-Erg	SVGFGNVS	112
M-Eag	SVGFGNIA	114
R-Eag	SVGFGNIA	114
Eag	SVGFGNVA	115
Elk	SVGFGNVS	112
Shaker	TVGYGDMT	116

FIG. 14C

0073695-1440

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0047-5656-1340



FIG. 13A



FIG. 13B

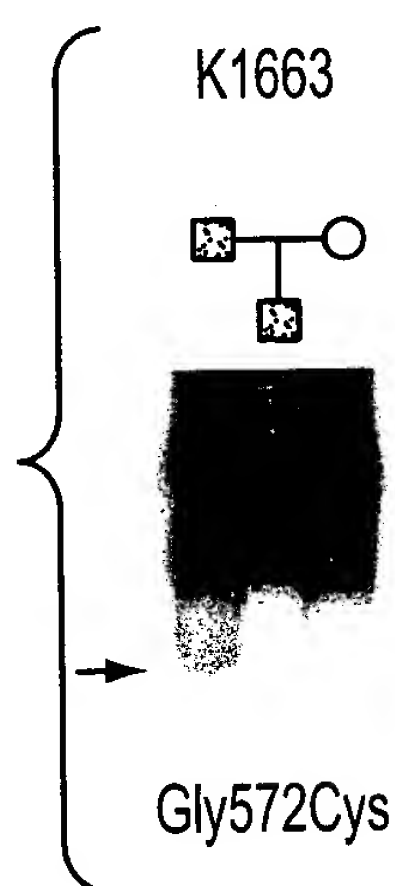


FIG. 13C

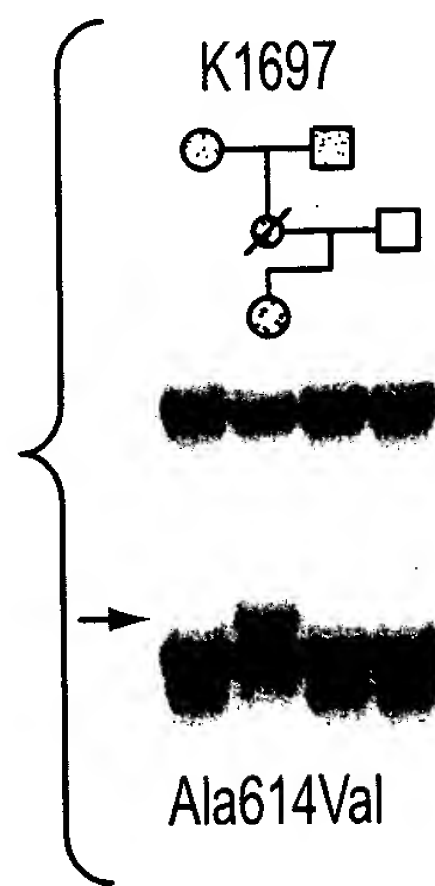


FIG. 13D

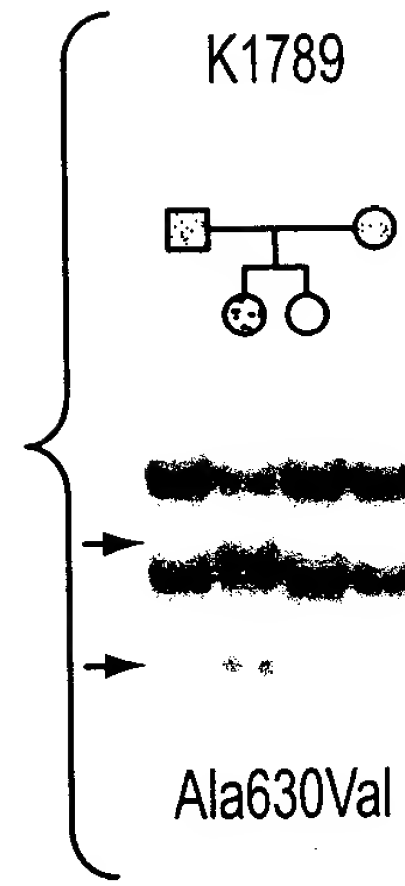
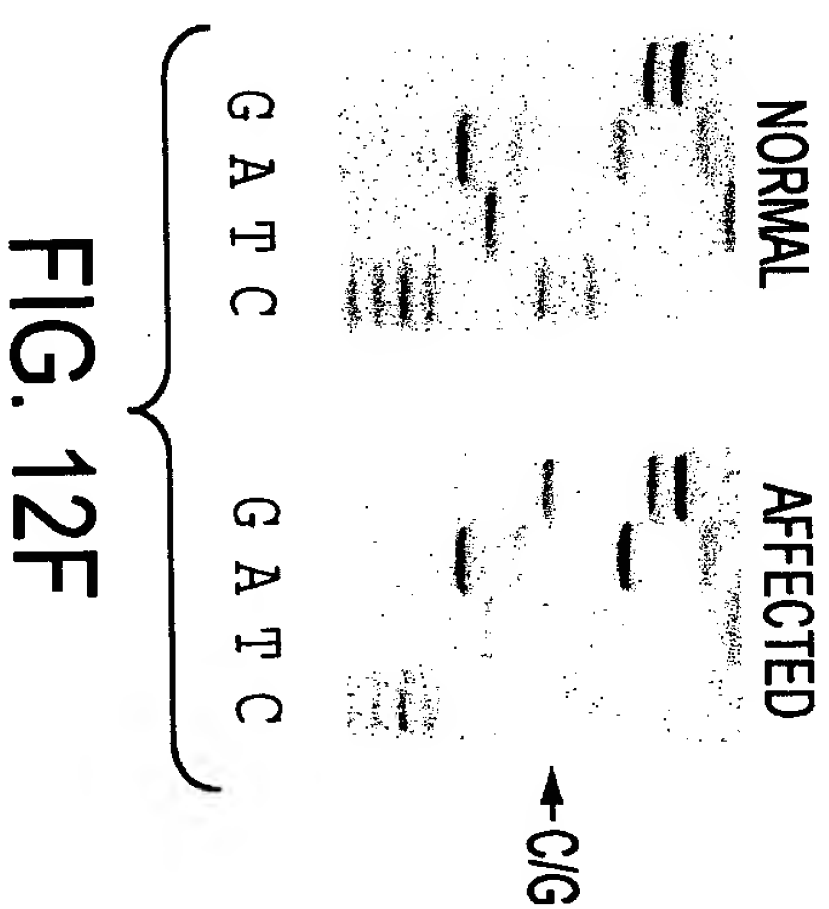
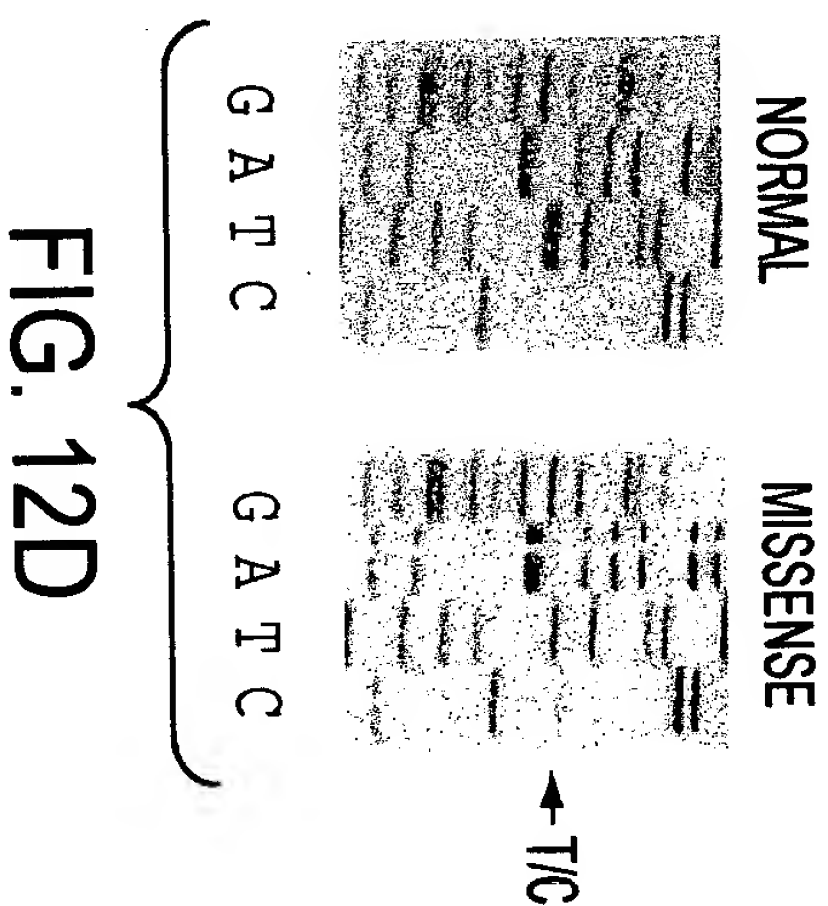
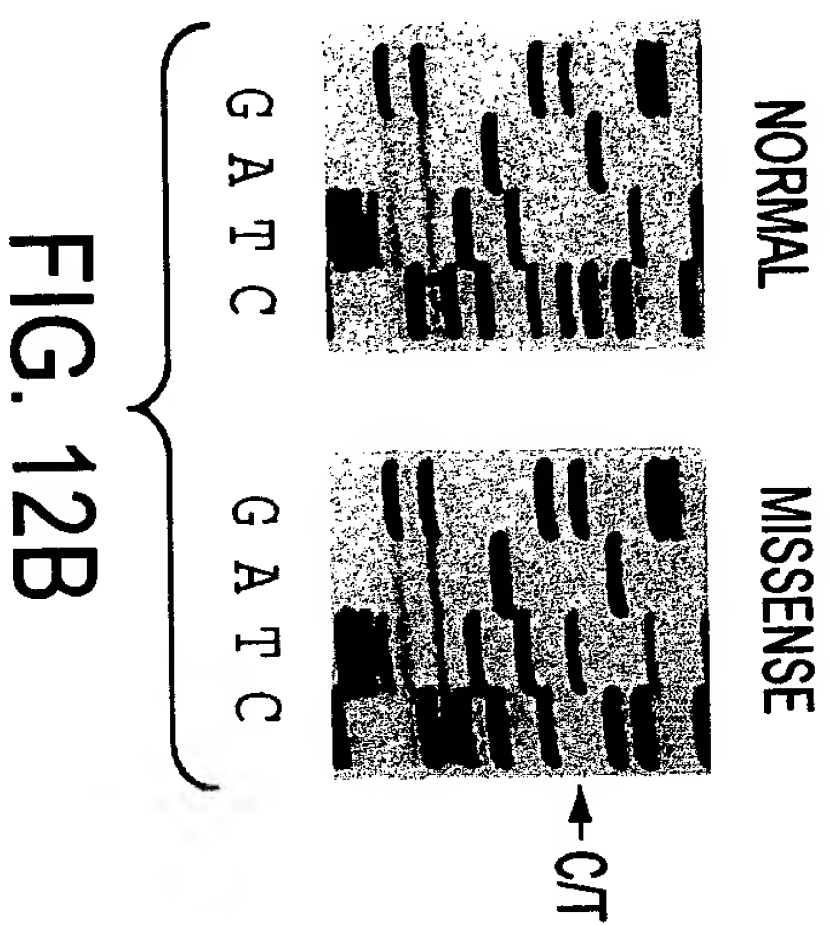
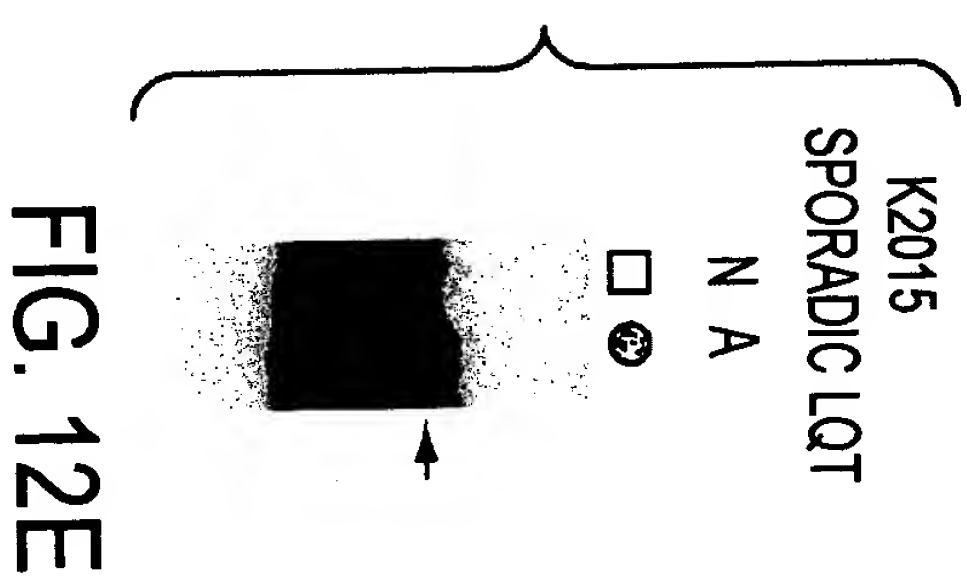
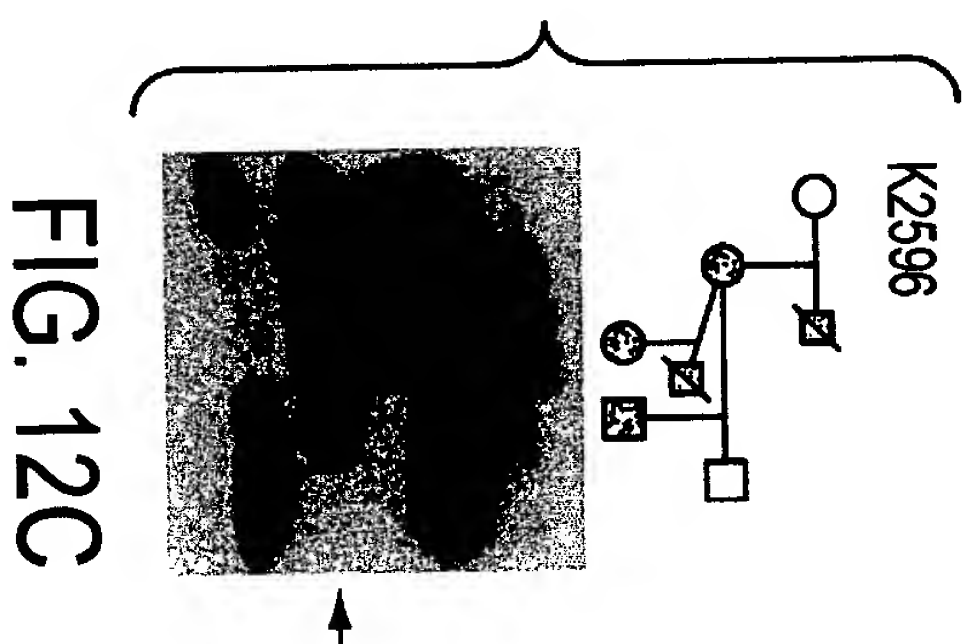
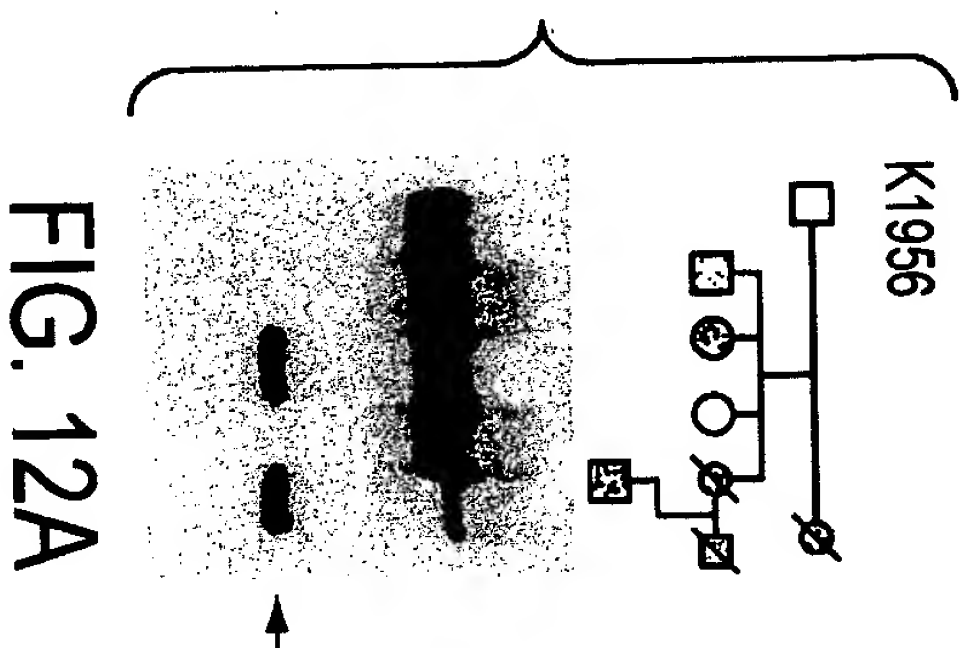


FIG. 13E



APPROVED	O.G. FIG.
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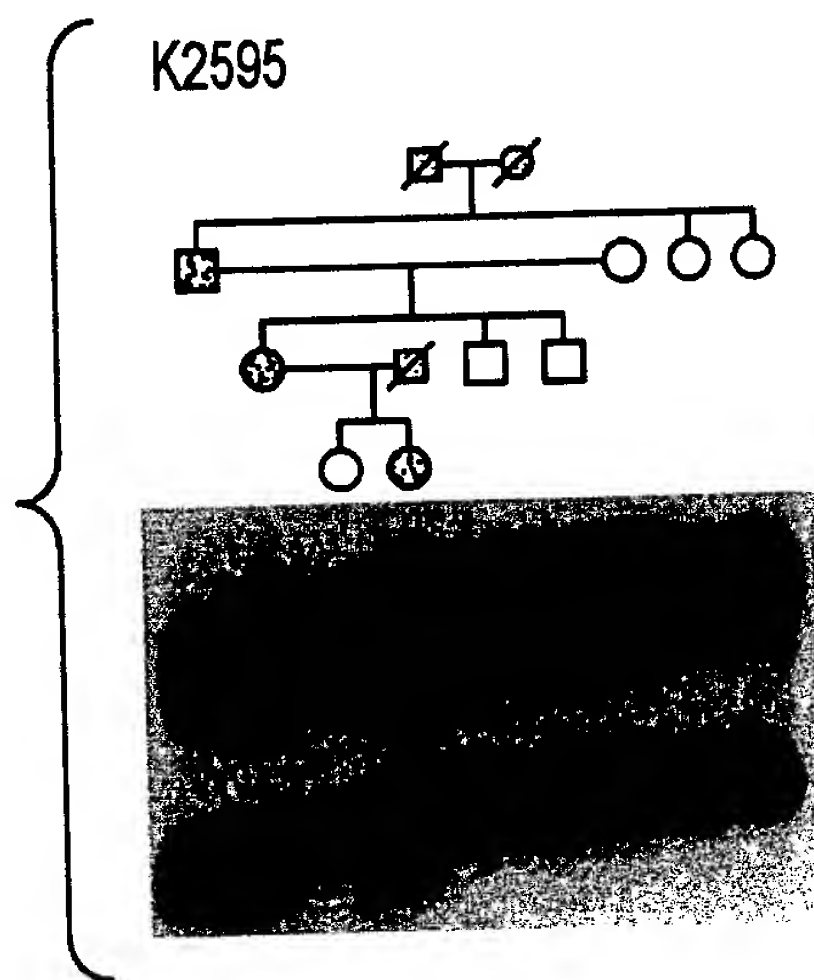


FIG. 11A

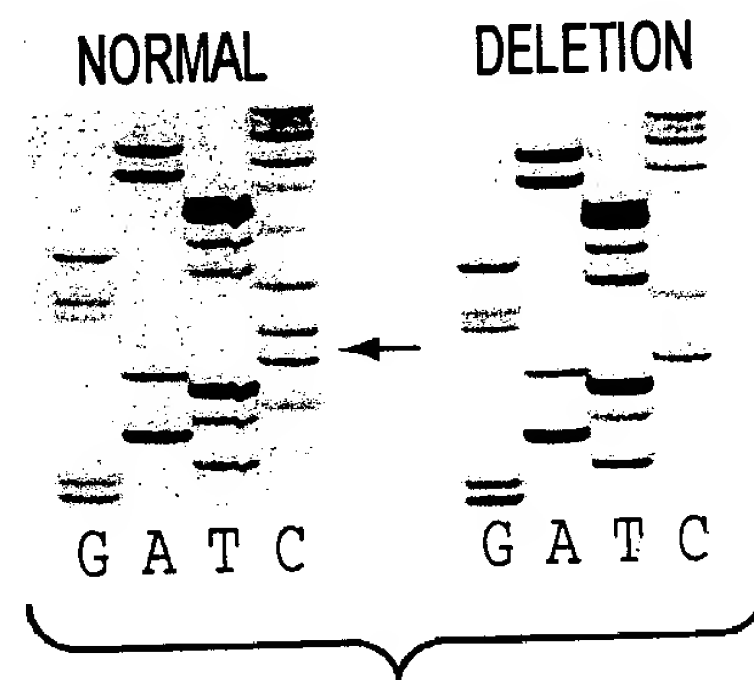


FIG. 11B